10001 11-608 207272

STIC-Biotech/ChemLib

From: Myers, Carla
Sent: Tuesday, November 14, 2006 7:29 AM
To: STIC-Biotech/ChemLib
Subject: sequence search for 10/823197

CAFE

Please search:
1) SEQ ID NO: 7
2) please perform a score over length search of SEQ ID NO: 7, with a minimum length of 8 nucleotides and a maximum length of 50 nucleotides, and a score over length cutoff of 70%.

Please provide an alignment in SCORE of the first 50 results (there is no need to provide a printed version of the results).

Thank you-

MR 17

Carla Myers
AU 1634
Remsen Bldg / Rm 2E79
Mailbox: REM 2C70
571-272-0747

MG

****
Searcher:_____
Searcher Phone:_____
Date Searcher Picked up:_____
Date completed:_____
Searcher Prep Time:_____
Online Time:_____

****
Type of Search
NA#_____ AA#:_____
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure #:_____Text:____
Inventor:_____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other (Specify):_____

Date completed: _____
Searcher: Beverly e2528
Terminal time: _____
Elapsed time: _____
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site
_____ STIC
_____ CM-1
_____ Pre-S

Type of Search
_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors
_____ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
✓ Other CGN

PTO-1590 (9-90)

Myers, C
10/823,197
Seq. ID 7

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: November 21, 2006, 14:27:35 ; Search time 0.001 Seconds
(without alignments)
60.656 Million cell updates/sec

Title: US-10-823-197-7
Perfect score: 17
Sequence: 1 CTCAGCAACACTCCTAT 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 156 seqs, 1784 residues

Total number of hits satisfying chosen parameters: 312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 156 summaries

Database : rgedb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	17	100.0	17	1	A82477	ACCESSION:A82477
	2	17	100.0	17	1	A84740	ACCESSION:A84740
	3	17	100.0	17	1	AR144074	ACCESSION:AR144074
	4	17	100.0	17	1	BD070852	ACCESSION:BD070852
	5	17	100.0	17	1	BD085841	ACCESSION:BD085841
	6	17	100.0	17	1	BD124538	ACCESSION:BD124538
	7	17	100.0	17	1	BD246771	ACCESSION:BD246771
	8	17	100.0	17	1	BD271249	ACCESSION:BD271249
	9	17	100.0	17	1	CQ918145	ACCESSION:CQ918145
	10	17	100.0	17	1	CS231184	ACCESSION:CS231184
	11	17	100.0	17	1	AR282877	ACCESSION:AR282877
	12	17	100.0	17	1	I85578	ACCESSION:I85578
	13	17	100.0	17	1	AR487085	ACCESSION:AR487085
	14	17	100.0	17	1	AR490513	ACCESSION:AR490513
	15	17	100.0	17	1	AR493814	ACCESSION:AR493814
	16	17	100.0	17	1	AR532946	ACCESSION:AR532946
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c 114	7.4	43.5	9	1	AX668904	ACCESSION:AX668904
c 115	7.4	43.5	9	1	AX668907	ACCESSION:AX668907
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c 128	7.4	43.5	10	1	BD239961	ACCESSION:BD239961
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131	7.4	43.5	10	1	CQ772480	ACCESSION:CQ772480
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c 148	7.4	43.5	10	1	AX152432	ACCESSION:AX152432
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ALIGNMENTS

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RESULT 1
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LOCUS       A82477                    17 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 15 from Patent WO9854359.
ACCESSION   A82477
VERSION     A82477.1  GI:6732221
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Duff,G. and Cox,A.
  TITLE     PREDICTION OF INFLAMMATORY DISEASE ASSOCIATED WITH IL-1 GENELOCI
            POLYMORPHISMS
  JOURNAL   Patent: WO 9854359-A 15 03-DEC-1998;
            DUFF GORDON (GB); COX ANGELA (GB)
FEATURES             Location/Qualifiers
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Qy          1 CTCAGCAACACTCCTAT 17
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Db          1 CTCAGCAACACTCCTAT 17


RESULT 2
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LOCUS       A84740                    17 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 1 from Patent WO9844150.
ACCESSION   A84740
VERSION     A84740.1  GI:6733608
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Spector,T.D. and Keen,R.W.
  TITLE     POLYMORPHISMS OF AN IL-1 RECEPTOR ANTAGONIST GENE
  JOURNAL   Patent: WO 9844150-A 1 08-OCT-1998;
            GEMINI RESEARCH LTD (GB); SPECTOR TIMOTHY DAVID (GB)
FEATURES             Location/Qualifiers
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RESULT 3
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LOCUS       AR144074                  17 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6210877.
ACCESSION   AR144074
VERSION     AR144074.1  GI:15105941
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Francis,S.E., Crossman,D.C. and Duff,G.W.
  TITLE     Prediction of coronary artery disease
  JOURNAL   Patent: US 6210877-A 1 03-APR-2001;
FEATURES             Location/Qualifiers
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Db          1 CTCAGCAACACTCCTAT 17


RESULT 4
BD070852
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LOCUS       BD070852                17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Prediction of coronary artery disease.
ACCESSION   BD070852
VERSION     BD070852.1  GI:22616455
KEYWORDS    JP 2001514522-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Francis,S.E., Crossman,D.C. and Duff,G.W.
  TITLE     Prediction of coronary artery disease
  JOURNAL   Patent: JP 2001514522-A 1 11-SEP-2001;
            INTERLEUKIN GENETICS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001514522-A/1
            PD   11-SEP-2001
            PF   09-MAR-1998 JP 1998539740
            PR   10-MAR-1997 US    08/813456
            PI   SHEILA E FRANCIS,DAVID C CROSSMAN,GORDON W DUFF PC
            C12Q1/68,C07H21/04,C12P19/34,G01N33/53
            CC   Primer for amplification of IL-1 RN
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Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 5
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LOCUS       BD085841                17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Methods of diagnosing and treating chronic obstructive airway
            diseases.
ACCESSION   BD085841
VERSION     BD085841.1  GI:22631451
KEYWORDS    JP 2001522586-A/5.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Duff,G.W., Giovain,M., Barnes,P.J. and Rim,S.
  TITLE     Methods of diagnosing and treating chronic obstructive airway
  JOURNAL   Patent: JP 2001522586-A 5 20-NOV-2001;
            INTERLEUKIN GENETICS INC
COMMENT     OS   Unidentified
            PN   JP 2001522586-A/5
            PD   20-NOV-2001
            PF   09-NOV-1998 JP 2000519607
            PR   07-NOV-1997 GB    9723553.5,12-JAN-1998 US    09/005923 PI
            GORDON W DUFF,MARKO GIOVAIN,PETER J BARNES,SIMON RIM PC
            C12N15/09,C12Q1/68,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Methods of diagnosing and treating chronic obstructive airway
            CC           diseases
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FEATURES             Location/Qualifiers
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Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 6
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LOCUS       BD124538                17 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Prediction of inflammatory disease associated with IL-1 geneloci
            polymorphisms.
ACCESSION   BD124538
VERSION     BD124538.1  GI:23219483
KEYWORDS    JP 2002500513-A/15.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Duff,G., Cox,A., Camp,N.J. and Giovine,F.S.D.
  TITLE     Prediction of inflammatory disease associated with IL-1 geneloci
            polymorphisms
  JOURNAL   Patent: JP 2002500513-A 15 08-JAN-2002;
            INTERLEUKIN GENETICS INC
COMMENT     OS   Unidentified
            PN   JP 2002500513-A/15
            PD   08-JAN-2002
            PF   21-MAY-1998 JP 1999500358
            PR   29-MAY-1997 GB    9711040.7
            PI   GORDON DUFF,ANGELA COX,NICOLA JANE CAMP,FRANCESCO SAVERIO DE
            PI   GIOVINE
            PC   C12Q1/68
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Prediction of inflammatory disease associated with IL-1  CC
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            CC   polymorphisms
            FH   Key             Location/Qualifiers
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Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 7
BD246771
LOCUS       BD246771                17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Diagnostics and therapeutics for sepsis.
ACCESSION   BD246771
VERSION     BD246771.1  GI:33056541
KEYWORDS    JP 2002533096-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Giovine,F.S.D. and Duff,G.W.
  TITLE     Diagnostics and therapeutics for sepsis
  JOURNAL   Patent: JP 2002533096-A 1 08-OCT-2002;
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            INTERLEUKIN GENETICS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002533096-A/1
            PD   08-OCT-2002
            PF   01-NOV-1999 JP 2000589732
            PR   30-OCT-1998 US    09/183850
            PI   FRANCESCO S DI GIOVINE,GORDON W DUFF
            PC   C12N15/09,A61K38/00,A61K45/00,A61P31/00,C12Q1/68,C12N15/00, PC
              A61K37/02
            CC   Description of Artificial Sequence: primer
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 8
BD271249
LOCUS       BD271249                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Prediction of risk of interstitial lung disease.
ACCESSION   BD271249
VERSION     BD271249.1  GI:33081017
KEYWORDS    JP 2002540801-A/21.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Duff,G.W., Giovine,F.S.D. and Whyte,M.
  TITLE     Prediction of risk of interstitial lung disease
  JOURNAL   Patent: JP 2002540801-A 21 03-DEC-2002;
            INTERLEUKIN GENETICS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002540801-A/21
            PD   03-DEC-2002
            PF   31-MAR-2000 JP 2000609606
            PR   02-APR-1999 US    09/286108
            PI   GORDON W DUFF,FRANCESCO SAVERIO DI GIOVINE,MORIA WHYTE PC
            C12N15/09,A61K31/57,A61K31/7088,A61K38/00,A61K45/00,A61K48/00, PC
            A61P11/00,
            PC   C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   A61K37/02
            CC   Description of Artificial Sequence: primer
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 9
CQ918145
LOCUS       CQ918145                 17 bp    DNA     linear   PAT 23-NOV-2004
DEFINITION  Sequence 29 from Patent WO2004097045.
ACCESSION   CQ918145
VERSION     CQ918145.1  GI:56208292
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Brown,M.A.
  TITLE     Diagnostic assay for ankylosing spondylitis
  JOURNAL   Patent: WO 2004097045-A 29 11-NOV-2004;
            ISIS INNOVATION LIMITED (GB)
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Primer"

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 10
CS231184
LOCUS       CS231184                 17 bp    DNA     linear   PAT 15-DEC-2005
DEFINITION  Sequence 22 from Patent WO2005108619.
ACCESSION   CS231184
VERSION     CS231184.1  GI:83698459
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Duff,G.W.
  TITLE     Diagnostics and therapeutics for diseases associated with an
            il-1inflammatory haplotype
  JOURNAL   Patent: WO 2005108619-A 22 17-NOV-2005;
            Interleukin Genetics, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Description of Artificial Sequence: chemically
                      synthesized primer"

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  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 11
AR282877
LOCUS       AR282877                 17 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 1 from patent US 6524795.
ACCESSION   AR282877
VERSION     AR282877.1  GI:29719679
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
```

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            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Francis,S.E., Crossman,D.C., Duff,G.W., Kornman,K.S. and
            Stephenson,K.
  TITLE     Diagnostics for cardiovascular disorders
  JOURNAL   Patent: US 6524795-A 1 25-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 12
I85578
LOCUS       I85578                  17 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 1 from patent US 5698399.
ACCESSION   I85578
VERSION     I85578.1  GI:3205296
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Duff,G.W., Russell,G. and Eastell,R.
  TITLE     Detecting genetic predisposition for osteoporosis
  JOURNAL   Patent: US 5698399-A 1 16-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 13
AR487085
LOCUS       AR487085                17 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 22 from patent US 6706478.
ACCESSION   AR487085
VERSION     AR487085.1  GI:47252036
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Duff,G.W., Cox,A., Camp,N.J. and di Giovine,F.S.
  TITLE     Diagnostics and therapeutics for diseases associated with an IL-1
            inflammatory haplotype
  JOURNAL   Patent: US 6706478-A 22 16-MAR-2004;
            Interleukin Genetics, Inc.; Waltham, MA;
            GBX;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 14
AR490513
LOCUS       AR490513                17 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 5 from patent US 6713253.
ACCESSION   AR490513
VERSION     AR490513.1  GI:47257894
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Duff,G.W., Richardson,P.R.S. and Rennie,I.G.
  TITLE     Detecting genetic predisposition to sight-threatening diabetic
            retinopathy
  JOURNAL   Patent: US 6713253-A 5 30-MAR-2004;
            Interleukin Genetics, Inc.; Waltham, MA;
            GBX;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 15
AR493814
LOCUS       AR493814                17 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 7 from patent US 6720141.
ACCESSION   AR493814
VERSION     AR493814.1  GI:47266264
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Crossman,D.C., Duff,G.W., Francis,S.E., Kornman,K.S. and
            Stephenson,K.
  TITLE     Diagnostics and therapeutics for restenosis
  JOURNAL   Patent: US 6720141-A 7 13-APR-2004;
            Interleukin Genetics, Inc.; Waltham, MA
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 16
AR532946
LOCUS       AR532946                17 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 9 from patent US 6730476.
ACCESSION   AR532946
VERSION     AR532946.1  GI:53922498
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Duff,G., Kornman,K. and van Dijk,S.
  TITLE     Methods of diagnosing early-onset menopause
  JOURNAL   Patent: US 6730476-A 9 04-MAY-2004;
            Interleukin Genetics, Inc.; Waltham, MA
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 17
AR534188
LOCUS       AR534188                  17 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 15 from patent US 6733967.
ACCESSION   AR534188
VERSION     AR534188.1  GI:53924221
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kornman,K.S., Duff,G.W. and Offenbacher,S.
  TITLE     Fetal testing for prediction of low birth weight
  JOURNAL   Patent: US 6733967-A 15 11-MAY-2004;
            Interleukin Genetics, Inc. and The University of North Carolina at
            Chapel Hill; Waltham, MA
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 18
AR542777
LOCUS       AR542777                  17 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 13 from patent US 6746839.
ACCESSION   AR542777
VERSION     AR542777.1  GI:53935453
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Duff,G.W., di Giovine,F.S., Barnes,P.J. and Lim,S.
  TITLE     Diagnostics and therapeutics for an obstructive airway disease
  JOURNAL   Patent: US 6746839-A 13 08-JUN-2004;
            Interleukin Genetics, Inc.; Waltham, MA
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 19
AX012493
LOCUS       AX012493                  17 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 9 from Patent WO9954499.
ACCESSION   AX012493
VERSION     AX012493.1  GI:9998491
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Harvey,W.
  TITLE     Method of analysis of chronic wounds
  JOURNAL   Patent: WO 9954499-A 9 28-OCT-1999;
            JOHNSON & JOHNSON MEDICAL LTD (GB); HARVEY WILSON (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer used in analysis for IL-IRN (intron 2)"

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 20
AX052797
LOCUS       AX052797                  17 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 7 from Patent WO0071753.
ACCESSION   AX052797
VERSION     AX052797.1  GI:12226954
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kornman,K.S., Duff,G.W., Crossman,D.C., Francis,S.E. and
            Stephenson,K.
  TITLE     Diagnostics and therapeutics for restenosis
  JOURNAL   Patent: WO 0071753-A 7 30-NOV-2000;
            Interleukin Genetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide used for PCR amplification"

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 21
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AX067286
LOCUS       AX067286                17 bp    DNA     linear   PAT 24-JAN-2001
DEFINITION  Sequence 22 from Patent WO0100880.
ACCESSION   AX067286
VERSION     AX067286.1  GI:12544910
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Duff,G.W., Cox,A., Camp,N.J. and di Giovine,F.S.
  TITLE     Diagnostics and therapeutics for diseases associated with an il-1
            inflammatory haplotype
  JOURNAL   Patent: WO 0100880-A 22 04-JAN-2001;
            Interleukin Genetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer"

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 22
AX360017
LOCUS       AX360017                17 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 3 from Patent WO0200933.
ACCESSION   AX360017
VERSION     AX360017.1  GI:18675643
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Duff,G.W. and Kornman,K.S.
  TITLE     Screening assays for identifying modulators of the inflammatory or
            immune responses
  JOURNAL   Patent: WO 0200933-A 3 03-JAN-2002;
            Interleukin Genetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 8;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 23
AR045302/c
LOCUS       AR045302                15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 95 from patent US 5817796.
ACCESSION   AR045302
VERSION     AR045302.1  GI:5966767
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb ribozymes having 2'-5'-linked adenylate residues
  JOURNAL   Patent: US 5817796-A 95 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             63.5%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 47;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCC 14
              |||||||||| | |
Db         14 CTCAGCAACAATTC 1


RESULT 24
I52354/c
LOCUS       I52354                  15 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 95 from patent US 5646042.
ACCESSION   I52354
VERSION     I52354.1  GI:2473555
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb targeted ribozymes
  JOURNAL   Patent: US 5646042-A 95 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             63.5%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 47;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCC 14
              |||||||||| | |
Db         14 CTCAGCAACAATTC 1


RESULT 25
AX587048/c
LOCUS       AX587048                15 bp    DNA     linear   PAT 10-JAN-2003
DEFINITION  Sequence 70 from Patent WO02072883.
ACCESSION   AX587048
VERSION     AX587048.1  GI:27655923
KEYWORDS    .
SOURCE      Saccharomyces cerevisiae (baker's yeast)
  ORGANISM  Saccharomyces cerevisiae
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1
  AUTHORS   Roetger,A.
  TITLE     Nucleotide carrier for diagnosing and treating oral diseases
  JOURNAL   Patent: WO 02072883-A 70 19-SEP-2002;
            ROETGER, Antje (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Saccharomyces cerevisiae"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:4932"

  Query Match             63.5%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 47;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 AGCAACACTCCTAT 17
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              ||| ||| ||||||
Db         15 AGCTACATTCCTAT 2


RESULT 26
CS097739/c
LOCUS       CS097739                  10 bp    DNA     linear   PAT 03-JUN-2005
DEFINITION  Sequence 12 from Patent EP1500329.
ACCESSION   CS097739
VERSION     CS097739.1  GI:66954141
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Green,L., Jakobovits,A., Klapholz,S., Kucherlapati,R. and Mendez,M.
  TITLE     Transgenic mammals having human Ig loci including plural VH and
            Vkappa regions and antibodies produced therefrom
  JOURNAL   Patent: EP 1500329-A 12 26-JAN-2005;
            Abgenix, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             58.8%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 AACACTCCTA 16
              ||||||||||
Db         10 AACACTCCTA 1


RESULT 27
AX470950/c
LOCUS       AX470950                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 527 from Patent WO02053773.
ACCESSION   AX470950
VERSION     AX470950.1  GI:22206075
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 527 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             55.3%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 37;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CAGCAACACTC 13
              |||||||| ||
Db         11 CAGCAACAGTC 1


RESULT 28
AX625650/c
LOCUS       AX625650                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2691 from Patent WO02053774.
ACCESSION   AX625650
VERSION     AX625650.1  GI:28453591
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2691 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             55.3%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 37;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CAGCAACACTC 13
              |||||||| ||
Db         11 CAGCAACAGTC 1


RESULT 29
BD124315/c
LOCUS       BD124315                  11 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Compositions and method for healing wound.
ACCESSION   BD124315
VERSION     BD124315.1  GI:23219260
KEYWORDS    JP 2002503460-A/146.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Katz,E.H.
  TITLE     Compositions and method for healing wound
  JOURNAL   Patent: JP 2002503460-A 146 05-FEB-2002;
            THE WISTAR INSTITUTE
COMMENT     OS   Mus musculus (mouse)
            PN   JP 2002503460-A/146
            PD   05-FEB-2002
            PF   12-FEB-1999 JP 2000531545
            PR   13-FEB-1998 US    60/074737,26-AUG-1998 US    60/097937 PR
            28-SEP-1998 US    60/102051
            PI   ELLEN HEBER KATZ
            PC   C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
              C12N5/00
            CC   Compositions and method for healing wound
            FH   Key             Location/Qualifiers
            FT   source          1. .11
            FT                   /organism='Mus musculus (mouse)'.
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"

  Query Match             52.9%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAAC 9
              |||||||||
Db          9 CTCAGCAAC 1
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RESULT 30
AR301565/c
LOCUS       AR301565                  11 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 146 from patent US 6538173.
ACCESSION   AR301565
VERSION     AR301565.1  GI:31689367
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Heber-Katz,E.
  TITLE     Compositions and methods for wound healing
  JOURNAL   Patent: US 6538173-A 146 25-MAR-2003;
            The Wistar Institute; Philadelphia, PA;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match           52.9%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity  100.0%;  Pred. No. 42;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAAC 9
              |||||||||
Db          9 CTCAGCAAC 1


RESULT 31
AR322159
LOCUS       AR322159                  12 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 10 from patent US 6566061.
ACCESSION   AR322159
VERSION     AR322159.1  GI:33707703
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Philibert,R.A., Ginns,E.I. and Delisi,L.
  TITLE     Identification of polymorphisms in the PCTG4 region of Xq13
  JOURNAL   Patent: US 6566061-A 10 20-MAY-2003;
            The University of Iowa, as represented by the University of Iowa
            Research Foundation and The United States of America as represented
            by the Department of Health and Human Services; Iowa City, IA
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match           52.9%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity  100.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CAGCAACAC 11
              |||||||||
Db          1 CAGCAACAC 9


RESULT 32
BD239508
LOCUS       BD239508                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239508
VERSION     BD239508.1  GI:33049278
KEYWORDS    JP 2002534056-A/926.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 926 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/926
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match           49.4%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity  90.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACA 10
              ||||||| |
Db          1 CTCAGCAAAA 10


RESULT 33
BD239610/c
LOCUS       BD239610                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239610
VERSION     BD239610.1  GI:33049380
KEYWORDS    JP 2002534056-A/1028.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1028 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/1028
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
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            19-JUN-1998 US     60/090035,19-JUN-1998 US     60/089993 PR
            19-JUN-1998 US     60/089992,19-JUN-1998 US     60/090072 PR
            19-JUN-1998 US     60/089878,19-JUN-1998 US     60/089991 PR
            19-JUN-1998 US     60/090000,19-JUN-1998 US     60/090048 PR
            19-JUN-1998 US     60/089999,19-JUN-1998 US     60/090043 PR
            19-JUN-1998 US     60/090042,19-JUN-1998 US     60/090036 PR
            19-JUN-1998 US     60/090044,19-JUN-1998 US     60/089844 PR
            19-JUN-1998 US     60/090080,19-JUN-1998 US     60/089833 PR
            19-JUN-1998 US     60/089994,19-JUN-1998 US     60/090077 PR
            19-JUN-1998 US     60/090078,19-JUN-1998 US     60/090047 PR
            19-JUN-1998 US     60/090076,19-JUN-1998 US     60/090045 PR
            08-DEC-1998 US     60/111715
            PI    BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC    C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC    C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC    C12N15/00,C12N5/00,C12N15/00
            CC    Preparation and use of superior vaccines
            FH    Key             Location/Qualifiers
            FT    source          1. .10
            FT                    /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             49.4%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACA 10
              ||||| ||||
Db         10 CTCAGGAACA 1


RESULT 34
CQ944980
LOCUS       CQ944980                  10 bp    DNA     linear   PAT 01-DEC-2004
DEFINITION  Sequence 127 from Patent WO2004099445.
ACCESSION   CQ944980
VERSION     CQ944980.1  GI:56294321
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kahl,G., Winter,P., Krueger,D., Reich,S., Matsumura,H. and
            Terauchi,R.
  TITLE     Use of a type iii restriction enzyme to isolate identification tags
            comprising more than 25 nucleotides
  JOURNAL   Patent: WO 2004099445-A 127 18-NOV-2004;
            Iwate Prefectual Government (JP)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence:Synthetic DNA
                     (Tag Sequence)"

  Query Match             49.4%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CAGCAACACT 12
              |||||| |||
Db          1 CAGCAATACT 10


RESULT 35
AX153002
LOCUS       AX153002                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 917 from Patent WO0138577.
ACCESSION   AX153002
VERSION     AX153002.1  GI:14534653
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 917 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             49.4%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCT 15
              ||||| ||||
Db          1 CAACATTCCT 10


RESULT 36
AX377359
LOCUS       AX377359                  10 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 23 from Patent WO0212499.
ACCESSION   AX377359
VERSION     AX377359.1  GI:19573645
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kliem,S.E., Koshy,B. and Lanz,E.M.
  TITLE     Haplotypes of the ntf3 gene
  JOURNAL   Patent: WO 0212499-A 23 14-FEB-2002;
            Genaissance Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             49.4%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 41;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GCAACACTCC 14
              ||||| ||||
Db          1 GCAACTCTCC 10


RESULT 37
CQ832726/c
LOCUS       CQ832726                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 97 from Patent WO2004059002.
ACCESSION   CQ832726
VERSION     CQ832726.1  GI:50832333
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining the homeostasis of hairy skin
  JOURNAL   Patent: WO 2004059002-A 97 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             49.4%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACA 10
              |.||||||||
Db         11 CCCAGCAACA 2


RESULT 38
CQ833174/c
LOCUS       CQ833174                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 545 from Patent WO2004059002.
ACCESSION   CQ833174
VERSION     CQ833174.1  GI:50832781
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining the homeostasis of hairy skin
  JOURNAL   Patent: WO 2004059002-A 545 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             49.4%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CAGCAACACT 12
              |||||| |||
Db         10 CAGCAAAACT 1


RESULT 39
CQ835198
LOCUS       CQ835198                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 256 from Patent WO2004059001.
ACCESSION   CQ835198
VERSION     CQ835198.1  GI:50834732
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining markers of human facial skin
  JOURNAL   Patent: WO 2004059001-A 256 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             49.4%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GCAACACTCC 14
              |||| |||||
Db          1 GCAAAACTCC 10


RESULT 40
CS058107
LOCUS       CS058107                  11 bp    DNA     linear   PAT 13-APR-2005
DEFINITION  Sequence 4 from Patent WO2005028671.
ACCESSION   CS058107
VERSION     CS058107.1  GI:62551059
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
            Kessler-Becker,D.
  TITLE     Method for determining hair cycle markers
  JOURNAL   Patent: WO 2005028671-A 4 31-MAR-2005;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             49.4%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCT 15
              ||||| ||||
Db          1 CAACATTCCT 10


RESULT 41
CS058332
LOCUS       CS058332                  11 bp    DNA     linear   PAT 13-APR-2005
DEFINITION  Sequence 229 from Patent WO2005028671.
ACCESSION   CS058332
VERSION     CS058332.1  GI:62551515
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
            Kessler-Becker,D.
  TITLE     Method for determining hair cycle markers
  JOURNAL   Patent: WO 2005028671-A 229 31-MAR-2005;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             49.4%;  Score 8.4;  DB 1;  Length 11;
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  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCT 15
              ||||| ||||
Db          1 CAACATTCCT 10


RESULT 42
AX623499
LOCUS       AX623499                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 540 from Patent WO02053774.
ACCESSION   AX623499
VERSION     AX623499.1  GI:28451440
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 540 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match            49.4%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GCAACACTCC 14
              |||| |||||
Db          1 GCAAGACTCC 10


RESULT 43
AX624606
LOCUS       AX624606                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 1647 from Patent WO02053774.
ACCESSION   AX624606
VERSION     AX624606.1  GI:28452547
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 1647 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

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  Best Local Similarity   90.0%;  Pred. No. 51;
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Qy          7 AACACTCCTA 16
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Db          1 AACATTCCTA 10


RESULT 44
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AX624745
LOCUS       AX624745                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 1786 from Patent WO02053774.
ACCESSION   AX624745
VERSION     AX624745.1  GI:28452686
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 1786 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match            49.4%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 AGCAACACTC 13
              || |||||||
Db          1 AGAAACACTC 10


RESULT 45
AX626573
LOCUS       AX626573                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3614 from Patent WO02053774.
ACCESSION   AX626573
VERSION     AX626573.1  GI:28454611
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3614 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match            49.4%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCT 15
              ||||| ||||
Db          1 CAACATTCCT 10


RESULT 46
AX627166
LOCUS       AX627166                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4207 from Patent WO02053774.
ACCESSION   AX627166
VERSION     AX627166.1  GI:28455204
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4207 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
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  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCT 15
              || |||||||
Db          1 CAGCACTCCT 10


RESULT 47
AX630920
LOCUS       AX630920                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7961 from Patent WO02053774.
ACCESSION   AX630920
VERSION     AX630920.1  GI:28458960
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7961 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             49.4%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GCAACACTCC 14
              |||| |||||
Db          1 GCAAGACTCC 10


RESULT 48
AX632027
LOCUS       AX632027                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 9069 from Patent WO02053774.
ACCESSION   AX632027
VERSION     AX632027.1  GI:28467642
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 9069 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             49.4%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 AACACTCCTA 16
              |||| |||||
Db          1 AACATTCCTA 10


RESULT 49
AX632166
LOCUS       AX632166                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 9208 from Patent WO02053774.
ACCESSION   AX632166
VERSION     AX632166.1  GI:28467781
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 9208 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             49.4%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 AGCAACACTC 13
              || |||||||
Db          1 AGAAACACTC 10


RESULT 50
AX708088/c
LOCUS       AX708088                  11 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 24 from Patent WO03014387.
ACCESSION   AX708088
VERSION     AX708088.1  GI:29564039
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Wojnowski,L. and Presecan-Siedel,E.
  TITLE     Polymorphisms in the human gene for cyp1a2 and their use in
            diagnostic and therapeutic applications
  JOURNAL   Patent: WO 03014387-A 24 20-FEB-2003;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             49.4%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ACACTCCTAT 17
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Db 10 ACCCTCCTAT 1

Search completed: November 21, 2006, 14:27:36
Job time : 1 secs

OM nucleic - nucleic search, using sw model

Run on: November 21, 2006, 14:29:06 ; Search time 0.001 Seconds
(without alignments)
214.472 Million cell updates/sec

Title: US-10-823-197-7
Perfect score: 17
Sequence: 1 CTCAGCAACACTCCTAT 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 513 seqs, 6308 residues

Total number of hits satisfying chosen parameters: 1026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 513 summaries

Database : rngdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	17	100.0	17	1	AAT89947	Human Interleukin-
	2	17	100.0	17	1	AAT89409	Human IL-1RN gene
	3	17	100.0	17	1	AAV62390	IL-1 receptor anta
	4	17	100.0	17	1	AAV60230	PCR primer used to
	5	17	100.0	17	1	AAV32393	Interleukin-1RN pr
	6	17	100.0	17	1	AAZ10706	PCR primer 1 used
	7	17	100.0	17	1	AAX75917	Human interleukin
	8	17	100.0	17	1	AAX16621	Interleukin 1 (441
	9	17	100.0	17	1	ABX15549	Human IL-1 genotyp
	10	17	100.0	17	1	AAZ37216	PCR primer for int
	11	17	100.0	17	1	AAA61915	Human IL-1RN (VNTR
	12	17	100.0	17	1	AAC63787	Human IL-1RN gene
	13	17	100.0	17	1	AAF27686	Primer #19. Unide
	14	17	100.0	17	1	AAC89171	Human IL-1RN (VNTR
	15	17	100.0	17	1	AAC91425	Human IL-1RN (VNTR
	16	17	100.0	17	1	AAD27377	PCR primer #1, use
	17	17	100.0	17	1	AAL54501	Ageing-related con
	18	17	100.0	17	1	AAD51455	Human interleukin-
	19	17	100.0	17	1	ADL83329	PCR primer #1for h
	20	17	100.0	17	1	ADN48846	Human secreted int
	21	17	100.0	17	1	ADO35276	Human interleukin-
	22	17	100.0	17	1	ADU16279	Human interleukin-
	23	17	100.0	17	1	ADU48041	Human IL-1A (VNTR)
	24	17	100.0	17	1	ADY72754	Human IL-1RN PCR p
	25	17	100.0	17	1	AEE01079	Human interleukin
	26	14	82.4	17	1	ACC44794	Interleukin 1 beta
	27	14	82.4	17	1	ADU50588	IL-1RN VNTR polymo
c	28	12.4	72.9	16	1	AAD48159	PCR primer #7 used
	29	12.4	72.9	17	1	ACN01682	WNV Inozyme substr
	30	12.4	72.9	17	1	ACN01683	WNV Inozyme substr
	31	12.4	72.9	17	1	ACN00198	WNV Hammerhead Rib
c	32	12.4	72.9	17	1	ACN14095	WNV minus strand D
c	33	12.4	72.9	17	1	ACN15151	WNV minus strand A
c	34	11	64.7	12	1	ABI02395	Oligonucleotide pr
	35	11	64.7	12	1	ABK72568	Human OPA1 gene, e
	36	11	64.7	13	1	ABF36021	Oligonucleotide SE
	37	11	64.7	13	1	ABC71077	Oligonucleotide SE
c	38	11	64.7	13	1	ABF36020	Oligonucleotide SE
c	39	11	64.7	13	1	ABC71076	Oligonucleotide SE
c	40	10.8	63.5	15	1	ABX03942	S. cerevisiae 28S
c	41	10.4	61.2	12	1	ABH90683	Oligonucleotide pr
c	42	10.4	61.2	12	1	ABI59938	Oligonucleotide pr
c	43	10.4	61.2	13	1	ABC51750	Oligonucleotide SE
c	44	10.4	61.2	13	1	ABF59814	Oligonucleotide SE
	45	10.4	61.2	13	1	ABF91047	Oligonucleotide SE
c	46	10.4	61.2	13	1	ABH23826	Oligonucleotide SE
c	47	10.4	61.2	13	1	ABF63332	Oligonucleotide SE
c	48	10.4	61.2	13	1	ABF79990	Oligonucleotide SE
	49	10.4	61.2	13	1	ABF63333	Oligonucleotide SE
	50	10.4	61.2	13	1	ABH62283	Oligonucleotide SE
	51	10.4	61.2	13	1	ABH22911	Oligonucleotide SE
c	52	10.4	61.2	13	1	ABF91046	Oligonucleotide SE
c	53	10.4	61.2	13	1	ABH51656	Oligonucleotide SE
c	54	10.4	61.2	13	1	ABH62282	Oligonucleotide SE
	55	10.4	61.2	13	1	ABH23827	Oligonucleotide SE
	56	10.4	61.2	13	1	ABC51751	Oligonucleotide SE
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	58	10.4	61.2	13	1	ABH51657	Oligonucleotide SE
c	59	10.4	61.2	13	1	ABH22910	Oligonucleotide SE
	60	10.4	61.2	13	1	ABF59815	Oligonucleotide SE
c	61	10	58.8	10	1	AAV42261	Clone B4.2.5 heavy
	62	10	58.8	12	1	ABI21932	Oligonucleotide pr
	63	10	58.8	12	1	ABI52691	Oligonucleotide pr
	64	10	58.8	12	1	ABI60262	Oligonucleotide pr
c	65	10	58.8	12	1	ABI75275	Oligonucleotide pr
	66	10	58.8	12	1	ABH80415	Oligonucleotide pr
c	67	10	58.8	12	1	ABI38816	Oligonucleotide pr
	68	10	58.8	12	1	ABI81630	Oligonucleotide pr
c	69	10	58.8	12	1	ABI31453	Oligonucleotide pr
	70	10	58.8	13	1	ABH42761	Oligonucleotide SE
c	71	10	58.8	13	1	ABC55542	Oligonucleotide SE
	72	10	58.8	13	1	ABC56303	Oligonucleotide SE
	73	10	58.8	13	1	ABF18025	Oligonucleotide SE
c	74	10	58.8	13	1	ABH27384	Oligonucleotide SE
	75	10	58.8	13	1	ABH27385	Oligonucleotide SE
	76	10	58.8	13	1	ABC56305	Oligonucleotide SE
	77	10	58.8	13	1	ABC55543	Oligonucleotide SE
c	78	10	58.8	13	1	ABC56302	Oligonucleotide SE
c	79	10	58.8	13	1	ABC56304	Oligonucleotide SE
c	80	10	58.8	13	1	ABC14326	Oligonucleotide SE
	81	10	58.8	13	1	ABC14327	Oligonucleotide SE
c	82	10	58.8	13	1	ABH42760	Oligonucleotide SE
c	83	10	58.8	13	1	ABF18024	Oligonucleotide SE
c	84	9.8	57.6	13	1	ABF74608	Oligonucleotide SE
	85	9.8	57.6	13	1	ABF06897	Oligonucleotide SE
c	86	9.8	57.6	13	1	ABF10496	Oligonucleotide SE
c	87	9.8	57.6	13	1	ABF23902	Oligonucleotide SE
	88	9.8	57.6	13	1	ABH09817	Oligonucleotide SE
c	89	9.8	57.6	13	1	ABH46274	Oligonucleotide SE
	90	9.8	57.6	13	1	ABF20671	Oligonucleotide SE
	91	9.8	57.6	13	1	ABF74609	Oligonucleotide SE
	92	9.8	57.6	13	1	ABF10497	Oligonucleotide SE
c	93	9.8	57.6	13	1	ABF20670	Oligonucleotide SE
c	94	9.8	57.6	13	1	ABC47162	Oligonucleotide SE
c	95	9.8	57.6	13	1	ABH09816	Oligonucleotide SE
	96	9.8	57.6	13	1	ABC47163	Oligonucleotide SE
	97	9.8	57.6	13	1	ABF23903	Oligonucleotide SE
	98	9.8	57.6	13	1	ABH46275	Oligonucleotide SE
c	99	9.8	57.6	13	1	ABF06896	Oligonucleotide SE
	100	9.6	56.5	13	1	ABF94757	Oligonucleotide SE
c	101	9.6	56.5	13	1	ABC01994	Oligonucleotide SE
	102	9.6	56.5	13	1	ABC01995	Oligonucleotide SE
c	103	9.6	56.5	13	1	ABF94756	Oligonucleotide SE
c	104	9.4	55.3	11	1	ABQ86772	Human skin stress/
c	105	9.4	55.3	11	1	ABV64905	Human skin EST 269
c	106	9.4	55.3	12	1	ABI27245	Oligonucleotide pr

c 107	9.4	55.3	12	1	ABH85429	Oligonucleotide pr
108	9.4	55.3	12	1	ABI59481	Oligonucleotide pr
c 109	9.4	55.3	12	1	ABI79256	Oligonucleotide pr
110	9.4	55.3	12	1	ABI13537	Oligonucleotide pr
111	9.4	55.3	12	1	ABH72484	Oligonucleotide pr
112	9.4	55.3	12	1	ABI70277	Oligonucleotide pr
c 113	9.4	55.3	12	1	ABI32479	Oligonucleotide pr
114	9.4	55.3	12	1	ABH83410	Oligonucleotide pr
c 115	9.4	55.3	12	1	ABH87181	Oligonucleotide pr
116	9.4	55.3	12	1	ABI51414	Oligonucleotide pr
117	9.4	55.3	12	1	ABH82860	Oligonucleotide pr
c 118	9.4	55.3	12	1	ABI38024	Oligonucleotide pr
119	9.4	55.3	12	1	ABI21294	Oligonucleotide pr
c 120	9.4	55.3	12	1	ABI21379	Oligonucleotide pr
121	9.4	55.3	12	1	ABI15864	Oligonucleotide pr
122	9.4	55.3	12	1	ABI69688	Oligonucleotide pr
c 123	9.4	55.3	12	1	ABH80014	Oligonucleotide pr
c 124	9.4	55.3	12	1	ABI79343	Oligonucleotide pr
c 125	9.4	55.3	13	1	ABF04402	Oligonucleotide SE
126	9.4	55.3	13	1	ABF69369	Oligonucleotide SE
c 127	9.4	55.3	13	1	ABH27108	Oligonucleotide SE
128	9.4	55.3	13	1	ABH48701	Oligonucleotide SE
c 129	9.4	55.3	13	1	ABC75386	Oligonucleotide SE
c 130	9.4	55.3	13	1	ABC86464	Oligonucleotide SE
c 131	9.4	55.3	13	1	ABF75706	Oligonucleotide SE
c 132	9.4	55.3	13	1	ABF53998	Oligonucleotide SE
133	9.4	55.3	13	1	ABH63333	Oligonucleotide SE
c 134	9.4	55.3	13	1	ABC71074	Oligonucleotide SE
135	9.4	55.3	13	1	ABC39629	Oligonucleotide SE
c 136	9.4	55.3	13	1	ABF79044	Oligonucleotide SE
c 137	9.4	55.3	13	1	ABH07982	Oligonucleotide SE
138	9.4	55.3	13	1	ABH33249	Oligonucleotide SE
c 139	9.4	55.3	13	1	ABH59110	Oligonucleotide SE
c 140	9.4	55.3	13	1	ABC24578	Oligonucleotide SE
141	9.4	55.3	13	1	ABF04403	Oligonucleotide SE
142	9.4	55.3	13	1	ABF08237	Oligonucleotide SE
143	9.4	55.3	13	1	ABF11811	Oligonucleotide SE
c 144	9.4	55.3	13	1	ABF69368	Oligonucleotide SE
145	9.4	55.3	13	1	ABF73021	Oligonucleotide SE
c 146	9.4	55.3	13	1	ABH35026	Oligonucleotide SE
147	9.4	55.3	13	1	ABC71085	Oligonucleotide SE
c 148	9.4	55.3	13	1	ABF08236	Oligonucleotide SE
c 149	9.4	55.3	13	1	ABC39628	Oligonucleotide SE
c 150	9.4	55.3	13	1	ABF27388	Oligonucleotide SE
151	9.4	55.3	13	1	ABF53293	Oligonucleotide SE
c 152	9.4	55.3	13	1	ABH33142	Oligonucleotide SE
153	9.4	55.3	13	1	ABC50881	Oligonucleotide SE
154	9.4	55.3	13	1	ABF17655	Oligonucleotide SE
155	9.4	55.3	13	1	ABF32705	Oligonucleotide SE
156	9.4	55.3	13	1	ABF36019	Oligonucleotide SE
c 157	9.4	55.3	13	1	ABH00132	Oligonucleotide SE
158	9.4	55.3	13	1	ABH00133	Oligonucleotide SE
c 159	9.4	55.3	13	1	ABH11456	Oligonucleotide SE
160	9.4	55.3	13	1	ABH11457	Oligonucleotide SE
c 161	9.4	55.3	13	1	ABF90352	Oligonucleotide SE
c 162	9.4	55.3	13	1	ABC96628	Oligonucleotide SE
c 163	9.4	55.3	13	1	ABC50880	Oligonucleotide SE
c 164	9.4	55.3	13	1	ABF36018	Oligonucleotide SE
165	9.4	55.3	13	1	ABF79045	Oligonucleotide SE
166	9.4	55.3	13	1	ABF53999	Oligonucleotide SE
167	9.4	55.3	13	1	ABH59111	Oligonucleotide SE
168	9.4	55.3	13	1	ABC71081	Oligonucleotide SE
169	9.4	55.3	13	1	ABC47373	Oligonucleotide SE
170	9.4	55.3	13	1	ABC86465	Oligonucleotide SE
171	9.4	55.3	13	1	ABH27109	Oligonucleotide SE
c 172	9.4	55.3	13	1	ABF53292	Oligonucleotide SE
173	9.4	55.3	13	1	ABH07983	Oligonucleotide SE
174	9.4	55.3	13	1	ABC86467	Oligonucleotide SE
175	9.4	55.3	13	1	ABF78085	Oligonucleotide SE
176	9.4	55.3	13	1	ABC00319	Oligonucleotide SE
177	9.4	55.3	13	1	ABF90353	Oligonucleotide SE
178	9.4	55.3	13	1	ABC71075	Oligonucleotide SE
c 179	9.4	55.3	13	1	ABC71084	Oligonucleotide SE
c 180	9.4	55.3	13	1	ABF78084	Oligonucleotide SE
c 181	9.4	55.3	13	1	ABF57068	Oligonucleotide SE
182	9.4	55.3	13	1	ABH35027	Oligonucleotide SE
c 183	9.4	55.3	13	1	ABH63332	Oligonucleotide SE
184	9.4	55.3	13	1	ABC42725	Oligonucleotide SE
c 185	9.4	55.3	13	1	ABC71080	Oligonucleotide SE
186	9.4	55.3	13	1	ABC24579	Oligonucleotide SE
c 187	9.4	55.3	13	1	ABC86466	Oligonucleotide SE
c 188	9.4	55.3	13	1	ABF32704	Oligonucleotide SE
189	9.4	55.3	13	1	ABH33143	Oligonucleotide SE
c 190	9.4	55.3	13	1	ABC42724	Oligonucleotide SE
c 191	9.4	55.3	13	1	ABC00318	Oligonucleotide SE
192	9.4	55.3	13	1	ABC25801	Oligonucleotide SE
193	9.4	55.3	13	1	ABF27385	Oligonucleotide SE
c 194	9.4	55.3	13	1	ABF73020	Oligonucleotide SE
c 195	9.4	55.3	13	1	ABH26572	Oligonucleotide SE
c 196	9.4	55.3	13	1	ABH48700	Oligonucleotide SE
197	9.4	55.3	13	1	ABC96629	Oligonucleotide SE
c 198	9.4	55.3	13	1	ABC25800	Oligonucleotide SE
199	9.4	55.3	13	1	ABC78901	Oligonucleotide SE
c 200	9.4	55.3	13	1	ABC62432	Oligonucleotide SE
201	9.4	55.3	13	1	ABF75707	Oligonucleotide SE
c 202	9.4	55.3	13	1	ABC47372	Oligonucleotide SE
c 203	9.4	55.3	13	1	ABC78900	Oligonucleotide SE
c 204	9.4	55.3	13	1	ABF17654	Oligonucleotide SE
c 205	9.4	55.3	13	1	ABF27384	Oligonucleotide SE
c 206	9.4	55.3	13	1	ABF74912	Oligonucleotide SE
207	9.4	55.3	13	1	ABH26573	Oligonucleotide SE
c 208	9.4	55.3	13	1	ABH27110	Oligonucleotide SE
209	9.4	55.3	13	1	ABH27111	Oligonucleotide SE
210	9.4	55.3	13	1	ABC75387	Oligonucleotide SE
c 211	9.4	55.3	13	1	ABF11810	Oligonucleotide SE
212	9.4	55.3	13	1	ABC62433	Oligonucleotide SE
213	9.4	55.3	13	1	ABF27389	Oligonucleotide SE
214	9.4	55.3	13	1	ABF74913	Oligonucleotide SE
215	9.4	55.3	13	1	ABF57069	Oligonucleotide SE
c 216	9.4	55.3	13	1	ABH33248	Oligonucleotide SE
c 217	9	52.9	10	1	AAZ84578	Metastatic breast
c 218	9	52.9	10	1	AAZ83877	Metastatic breast
c 219	9	52.9	10	1	AAZ86013	Metastatic breast
c 220	9	52.9	10	1	AAF39825	Yeast NORF gene SA
221	9	52.9	10	1	AAF41735	Yeast NORF gene SA
c 222	9	52.9	10	1	AAL44250	Human interleukin
c 223	9	52.9	11	1	AAZ18836	Murine C57BL/6 SAG
224	9	52.9	12	1	AAQ52017	B-cell mRNA ribozy
225	9	52.9	12	1	AAZ45605	A 12 bp polymorphi
c 226	9	52.9	12	1	ABI08527	Oligonucleotide pr
227	9	52.9	12	1	ABI18112	Oligonucleotide pr
c 228	9	52.9	12	1	ABI51111	Oligonucleotide pr
229	9	52.9	12	1	ABI52991	Oligonucleotide pr
230	9	52.9	12	1	ABI36091	Oligonucleotide pr
231	9	52.9	12	1	ABI09061	Oligonucleotide pr
232	9	52.9	12	1	ABI04541	Oligonucleotide pr
c 233	9	52.9	12	1	ABI31454	Oligonucleotide pr
234	9	52.9	12	1	ABI49286	Oligonucleotide pr
c 235	9	52.9	12	1	ABI18491	Oligonucleotide pr
236	9	52.9	12	1	ABH89063	Oligonucleotide pr
237	9	52.9	12	1	ABH74551	Oligonucleotide pr
238	8.8	51.8	12	1	ABI14113	Oligonucleotide pr
239	8.8	51.8	12	1	ABI69162	Oligonucleotide pr
240	8.8	51.8	12	1	ABI22817	Oligonucleotide pr
241	8.8	51.8	12	1	ABI43805	Oligonucleotide pr
242	8.8	51.8	12	1	ABI21129	Oligonucleotide pr
c 243	8.8	51.8	12	1	ABI03049	Oligonucleotide pr
244	8.8	51.8	12	1	ABI22041	Oligonucleotide pr
c 245	8.8	51.8	12	1	ABH82739	Oligonucleotide pr
246	8.8	51.8	12	1	ABI14114	Oligonucleotide pr
c 247	8.8	51.8	12	1	ABI70127	Oligonucleotide pr
248	8.8	51.8	12	1	ABH72016	Oligonucleotide pr
249	8.8	51.8	12	1	ABH90061	Oligonucleotide pr
250	8.8	51.8	12	1	ABH89055	Oligonucleotide pr
c 251	8.8	51.8	12	1	ABI53259	Oligonucleotide pr
c 252	8.8	51.8	12	1	ABI60527	Oligonucleotide pr

c 253	8.8	51.8	12	1	ABI74519	Oligonucleotide pr
c 254	8.8	51.8	12	1	ABI71780	Oligonucleotide pr
c 255	8.8	51.8	12	1	ABI07523	Oligonucleotide pr
256	8.8	51.8	12	1	ABI51318	Oligonucleotide pr
257	8.8	51.8	12	1	ABI21119	Oligonucleotide pr
c 258	8.8	51.8	12	1	ABI26465	Oligonucleotide pr
c 259	8.8	51.8	12	1	ABI29621	Oligonucleotide pr
c 260	8.8	51.8	12	1	ABI13441	Oligonucleotide pr
c 261	8.8	51.8	12	1	ABI67962	Oligonucleotide pr
c 262	8.8	51.8	12	1	ABI32800	Oligonucleotide pr
263	8.8	51.8	12	1	ABI52724	Oligonucleotide pr
c 264	8.8	51.8	12	1	ABI57315	Oligonucleotide pr
265	8.8	51.8	12	1	ABH70146	Oligonucleotide pr
266	8.8	51.8	12	1	ABH95774	Oligonucleotide pr
267	8.8	51.8	12	1	ABH98439	Oligonucleotide pr
268	8.8	51.8	12	1	ABH77746	Oligonucleotide pr
c 269	8.8	51.8	12	1	ABI62490	Oligonucleotide pr
c 270	8.8	51.8	12	1	ABI79845	Oligonucleotide pr
271	8.8	51.8	12	1	ABI79880	Oligonucleotide pr
272	8.8	51.8	12	1	ABI28200	Oligonucleotide pr
273	8.8	51.8	12	1	ABI52706	Oligonucleotide pr
274	8.8	51.8	12	1	ABI75840	Oligonucleotide pr
275	8.8	51.8	12	1	ABI07459	Oligonucleotide pr
276	8.8	51.8	12	1	ABH90883	Oligonucleotide pr
277	8.4	49.4	10	1	AAZ78498	Human dendritic ce
c 278	8.4	49.4	10	1	AAZ78600	Human dendritic ce
279	8.4	49.4	10	1	AAZ86614	Metastatic breast
280	8.4	49.4	10	1	AAZ84155	Metastatic breast
281	8.4	49.4	10	1	AAZ81494	Metastatic breast
282	8.4	49.4	10	1	AAZ84891	Metastatic breast
c 283	8.4	49.4	10	1	AAZ85466	Metastatic breast
284	8.4	49.4	10	1	AAZ85411	Metastatic breast
c 285	8.4	49.4	10	1	AAZ84473	Metastatic breast
286	8.4	49.4	10	1	AAH64077	Human ubiquitously
287	8.4	49.4	10	1	AAF35663	Yeast NORF gene SA
288	8.4	49.4	10	1	AAF37497	Yeast NORF gene SA
c 289	8.4	49.4	10	1	AAF34369	Yeast NORF gene SA
290	8.4	49.4	10	1	AAF40645	Yeast NORF gene SA
291	8.4	49.4	10	1	AAF36364	Yeast NORF gene SA
292	8.4	49.4	10	1	AAS18737	Primer-extension o
293	8.4	49.4	10	1	AAD32319	Human neurotrophin
c 294	8.4	49.4	10	1	ADU18500	Hypoxia-related tu
295	8.4	49.4	10	1	ADU18776	Hypoxia-related tu
296	8.4	49.4	10	1	ADU18606	Hypoxia-related tu
297	8.4	49.4	10	1	ADU78503	Rice oligonucleoti
298	8.4	49.4	11	1	ABV70175	Human skin EST 796
299	8.4	49.4	11	1	ABV62754	Human skin EST 540
300	8.4	49.4	11	1	ABV63861	Human skin EST 164
301	8.4	49.4	11	1	ABV64000	Human skin EST 178
302	8.4	49.4	11	1	ABV66421	Human skin EST 420
303	8.4	49.4	11	1	ABV71282	Human skin EST 906
304	8.4	49.4	11	1	ABV71421	Human skin EST 920
305	8.4	49.4	11	1	ABV65828	Human skin EST 361
c 306	8.4	49.4	11	1	ACC90658	Human CYP1A2 PCR p
c 307	8.4	49.4	11	1	ADQ35280	Human hair-bearing
c 308	8.4	49.4	11	1	ADQ35728	Human hair-bearing
309	8.4	49.4	11	1	ADQ32166	Human facial skin-
310	8.4	49.4	12	1	AAT80290	Oligo HCV-139, tar
311	8.4	49.4	12	1	AAZ41785	Organic material d
312	8.4	49.4	12	1	AAZ41569	Microbe detection
c 313	8.4	49.4	12	1	AAX88508	Gamma-conopeptide
c 314	8.4	49.4	12	1	AAZ34552	Putative Alfin1 bi
315	8.4	49.4	12	1	AAC97920	Primer used to ill
316	8.4	49.4	12	1	ABI19922	Oligonucleotide pr
317	8.4	49.4	12	1	ABH95281	Oligonucleotide pr
c 318	8.4	49.4	12	1	ABH75072	Oligonucleotide pr
c 319	8.4	49.4	12	1	ABI25291	Oligonucleotide pr
320	8.4	49.4	12	1	ABI04562	Oligonucleotide pr
c 321	8.4	49.4	12	1	ABI10726	Oligonucleotide pr
c 322	8.4	49.4	12	1	ABI36250	Oligonucleotide pr
323	8.4	49.4	12	1	ABI12735	Oligonucleotide pr
324	8.4	49.4	12	1	ABI73353	Oligonucleotide pr
325	8.4	49.4	12	1	ABI79465	Oligonucleotide pr
326	8.4	49.4	12	1	ABI20130	Oligonucleotide pr
c 327	8.4	49.4	12	1	ABI04273	Oligonucleotide pr
328	8.4	49.4	12	1	ABI32048	Oligonucleotide pr
c 329	8.4	49.4	12	1	ABI49461	Oligonucleotide pr
330	8.4	49.4	12	1	ABI50359	Oligonucleotide pr
331	8.4	49.4	12	1	ABI71640	Oligonucleotide pr
c 332	8.4	49.4	12	1	ABI58376	Oligonucleotide pr
333	8.4	49.4	12	1	ABI60263	Oligonucleotide pr
c 334	8.4	49.4	12	1	ABH85930	Oligonucleotide pr
335	8.4	49.4	12	1	ABI37591	Oligonucleotide pr
c 336	8.4	49.4	12	1	ABI49460	Oligonucleotide pr
337	8.4	49.4	12	1	ABI73802	Oligonucleotide pr
338	8.4	49.4	12	1	ABI23841	Oligonucleotide pr
c 339	8.4	49.4	12	1	ABH75074	Oligonucleotide pr
c 340	8.4	49.4	12	1	ABI26596	Oligonucleotide pr
c 341	8.4	49.4	12	1	ABI02634	Oligonucleotide pr
c 342	8.4	49.4	12	1	ABI05684	Oligonucleotide pr
c 343	8.4	49.4	12	1	ABI35125	Oligonucleotide pr
344	8.4	49.4	12	1	ABH85359	Oligonucleotide pr
c 345	8.4	49.4	12	1	ABI60784	Oligonucleotide pr
346	8.4	49.4	12	1	ABI62460	Oligonucleotide pr
c 347	8.4	49.4	12	1	ABH75244	Oligonucleotide pr
c 348	8.4	49.4	12	1	ABI08676	Oligonucleotide pr
c 349	8.4	49.4	12	1	ABH86879	Oligonucleotide pr
350	8.4	49.4	12	1	ABH89347	Oligonucleotide pr
351	8.4	49.4	12	1	ABI51514	Oligonucleotide pr
c 352	8.4	49.4	12	1	ABI52940	Oligonucleotide pr
353	8.4	49.4	12	1	ABI78050	Oligonucleotide pr
354	8.4	49.4	12	1	ABH83800	Oligonucleotide pr
355	8.4	49.4	12	1	ABI52587	Oligonucleotide pr
356	8.4	49.4	12	1	ABI65914	Oligonucleotide pr
c 357	8.4	49.4	12	1	ABH68170	Oligonucleotide pr
358	8.4	49.4	12	1	ABH71713	Oligonucleotide pr
359	8.4	49.4	12	1	ABI23582	Oligonucleotide pr
360	8.4	49.4	12	1	ABI23840	Oligonucleotide pr
361	8.4	49.4	12	1	ABI29757	Oligonucleotide pr
362	8.4	49.4	12	1	ABI35425	Oligonucleotide pr
363	8.4	49.4	12	1	ABH89609	Oligonucleotide pr
c 364	8.4	49.4	12	1	ABI52629	Oligonucleotide pr
365	8.4	49.4	12	1	ABI73498	Oligonucleotide pr
366	8.4	49.4	12	1	ABI76817	Oligonucleotide pr
367	8.4	49.4	12	1	ABI77369	Oligonucleotide pr
c 368	8.4	49.4	12	1	ABI65694	Oligonucleotide pr
369	8.4	49.4	12	1	ABI81322	Oligonucleotide pr
370	8.4	49.4	12	1	ABH71244	Oligonucleotide pr
c 371	8.4	49.4	12	1	ABI02874	Oligonucleotide pr
c 372	8.4	49.4	12	1	ABI04205	Oligonucleotide pr
373	8.4	49.4	12	1	ABI54050	Oligonucleotide pr
c 374	8.4	49.4	12	1	ABI61147	Oligonucleotide pr
c 375	8.4	49.4	12	1	ABI62277	Oligonucleotide pr
c 376	8.4	49.4	12	1	ABH93056	Oligonucleotide pr
c 377	8.4	49.4	12	1	ABH94308	Oligonucleotide pr
378	8.4	49.4	12	1	ABH71714	Oligonucleotide pr
379	8.4	49.4	12	1	ABI01047	Oligonucleotide pr
c 380	8.4	49.4	12	1	ABH80648	Oligonucleotide pr
381	8.4	49.4	12	1	ABI13133	Oligonucleotide pr
382	8.4	49.4	12	1	ABI42830	Oligonucleotide pr
383	8.4	49.4	12	1	ABI68945	Oligonucleotide pr
c 384	8.4	49.4	12	1	ABI62847	Oligonucleotide pr
c 385	8.4	49.4	12	1	ABI04637	Oligonucleotide pr
386	8.4	49.4	12	1	ABI33500	Oligonucleotide pr
c 387	8.4	49.4	12	1	ABI35127	Oligonucleotide pr
c 388	8.4	49.4	12	1	ABI36791	Oligonucleotide pr
c 389	8.4	49.4	12	1	ABI42330	Oligonucleotide pr
c 390	8.4	49.4	12	1	ABI72623	Oligonucleotide pr
c 391	8.4	49.4	12	1	ABI64366	Oligonucleotide pr
c 392	8.4	49.4	12	1	ABI79267	Oligonucleotide pr
393	8.4	49.4	12	1	ABI80201	Oligonucleotide pr
c 394	8.4	49.4	12	1	ABI02907	Oligonucleotide pr
395	8.4	49.4	12	1	ABI34125	Oligonucleotide pr
396	8.4	49.4	12	1	ABI37442	Oligonucleotide pr
c 397	8.4	49.4	12	1	ABI42471	Oligonucleotide pr
398	8.4	49.4	12	1	ABI47600	Oligonucleotide pr

c 399	8.4	49.4	12	1	ABI54882	Oligonucleotide pr
400	8.4	49.4	12	1	ABI78533	Oligonucleotide pr
401	8.4	49.4	12	1	ABH99854	Oligonucleotide pr
c 402	8.4	49.4	12	1	ABI05412	Oligonucleotide pr
403	8.4	49.4	12	1	ABI10692	Oligonucleotide pr
c 404	8.4	49.4	12	1	ABH91733	Oligonucleotide pr
405	8.4	49.4	12	1	ABI72865	Oligonucleotide pr
406	8.4	49.4	12	1	ABI74449	Oligonucleotide pr
c 407	8.4	49.4	12	1	ABI21004	Oligonucleotide pr
c 408	8.4	49.4	12	1	ABH88530	Oligonucleotide pr
c 409	8.4	49.4	12	1	ABH89232	Oligonucleotide pr
410	8.4	49.4	12	1	ABH89348	Oligonucleotide pr
411	8.4	49.4	12	1	ABI39892	Oligonucleotide pr
c 412	8.4	49.4	12	1	ABI15535	Oligonucleotide pr
413	8.4	49.4	12	1	ABI42757	Oligonucleotide pr
c 414	8.4	49.4	12	1	ABI56889	Oligonucleotide pr
415	8.4	49.4	12	1	ABI59223	Oligonucleotide pr
416	8.4	49.4	12	1	ABI75721	Oligonucleotide pr
417	8.4	49.4	12	1	ABI62250	Oligonucleotide pr
c 418	8.4	49.4	12	1	ABI78281	Oligonucleotide pr
c 419	8.4	49.4	12	1	ABH69839	Oligonucleotide pr
420	8.4	49.4	12	1	ABI21482	Oligonucleotide pr
c 421	8.4	49.4	12	1	ABH78310	Oligonucleotide pr
c 422	8.4	49.4	12	1	ABI28957	Oligonucleotide pr
c 423	8.4	49.4	12	1	ABI36589	Oligonucleotide pr
424	8.4	49.4	12	1	ABI38671	Oligonucleotide pr
425	8.4	49.4	12	1	ABI68149	Oligonucleotide pr
426	8.4	49.4	12	1	ABI76866	Oligonucleotide pr
c 427	8.4	49.4	12	1	ABH95121	Oligonucleotide pr
c 428	8.4	49.4	12	1	ABH70717	Oligonucleotide pr
c 429	8.4	49.4	12	1	ABI36041	Oligonucleotide pr
c 430	8.4	49.4	12	1	ABI38817	Oligonucleotide pr
431	8.4	49.4	12	1	ABI16173	Oligonucleotide pr
c 432	8.4	49.4	12	1	ABH91205	Oligonucleotide pr
433	8.4	49.4	12	1	ABI44592	Oligonucleotide pr
434	8.4	49.4	12	1	ABI61247	Oligonucleotide pr
435	8.4	49.4	12	1	ABI75722	Oligonucleotide pr
c 436	8.4	49.4	12	1	ABI76793	Oligonucleotide pr
c 437	8.4	49.4	12	1	ABI18065	Oligonucleotide pr
c 438	8.4	49.4	12	1	ABI22651	Oligonucleotide pr
c 439	8.4	49.4	12	1	ABH74400	Oligonucleotide pr
440	8.4	49.4	12	1	ABH99939	Oligonucleotide pr
441	8.4	49.4	12	1	ABH76541	Oligonucleotide pr
c 442	8.4	49.4	12	1	ABI04203	Oligonucleotide pr
c 443	8.4	49.4	12	1	ABI05195	Oligonucleotide pr
444	8.4	49.4	12	1	ABI08517	Oligonucleotide pr
c 445	8.4	49.4	12	1	ABH85347	Oligonucleotide pr
c 446	8.4	49.4	12	1	ABI50743	Oligonucleotide pr
447	8.4	49.4	12	1	ABI79869	Oligonucleotide pr
448	8.4	49.4	12	1	ABS65874	Inhibitory oligonu
449	8.4	49.4	12	1	ADF78583	Chromosomal abnorm
450	8.4	49.4	12	1	ADR98159	Human chromosome 2
451	8.4	49.4	12	1	ADS08846	Human DNA PCR prim
c 452	8	47.1	9	1	ABQ72166	Zinc finger protei
c 453	8	47.1	9	1	ABQ72165	Zinc finger protei
c 454	8	47.1	9	1	ADA64492	Zinc finger target
c 455	8	47.1	9	1	ADA64493	Zinc finger target
c 456	8	47.1	9	1	ADM23185	Synthetic zinc fin
c 457	8	47.1	9	1	ADM23184	Synthetic zinc fin
458	8	47.1	10	1	AAZ77970	Human dendritic ce
c 459	8	47.1	10	1	AAZ77979	Human dendritic ce
460	8	47.1	10	1	AAZ77719	Human dendritic ce
461	8	47.1	10	1	AAZ79289	Human dendritic ce
c 462	8	47.1	10	1	AAZ84195	Metastatic breast
463	8	47.1	10	1	AAH63313	Human keratinocyte
464	8	47.1	10	1	AAF34623	Yeast NORF gene SA
465	8	47.1	10	1	AAF33976	Yeast NORF gene SA
466	8	47.1	10	1	AAF35615	Yeast NORF gene SA
467	8	47.1	10	1	AAF41358	Yeast NORF gene SA
c 468	8	47.1	10	1	AAF42339	Yeast NORF gene SA
469	8	47.1	10	1	AAF39135	Yeast NORF gene SA
c 470	8	47.1	10	1	AAF35208	Yeast NORF gene SA
c 471	8	47.1	10	1	AAF36519	Yeast NORF gene SA
472	8	47.1	10	1	ABL01209	Human AKR1B1 gene
473	8	47.1	10	1	ABQ88699	Human CFL1 primer
c 474	8	47.1	10	1	ACC85197	Human prothrombin
475	8	47.1	10	1	ADU19523	Hypoxia-related tu
476	8	47.1	11	1	AAX24421	Bovine myostatin m
c 477	8	47.1	11	1	ABV64656	Human skin EST 244
c 478	8	47.1	11	1	ABV66565	Human skin EST 435
c 479	8	47.1	11	1	ABV71821	Human skin EST 960
480	8	47.1	11	1	ABV65947	Human skin EST 373
c 481	8	47.1	11	1	ABV64400	Human skin EST 218
c 482	8	47.1	11	1	ADQ32942	Human facial skin-
483	8	47.1	11	1	ADQ33462	Human facial skin-
484	8	47.1	11	1	ADR35386	Human nicking agen
485	8	47.1	11	1	ADR35383	Human nicking agen
486	8	47.1	11	1	ADR35385	Human nicking agen
487	8	47.1	11	1	ADR35384	Human nicking agen
488	8	47.1	11	1	ADZ23301	Human SNP detectio
c 489	7.8	45.9	11	1	ABQ87409	Human skin stress/
c 490	7.8	45.9	11	1	ABQ86753	Human skin stress/
c 491	7.8	45.9	11	1	ABV66019	Human skin EST 380
492	7.8	45.9	11	1	ABV69906	Human skin EST 769
493	7.8	45.9	11	1	ABV70411	Human skin EST 819
494	7.8	45.9	11	1	ABV62485	Human skin EST 271
495	7.8	45.9	11	1	ABV62990	Human skin EST 776
c 496	7.8	45.9	11	1	ABV64563	Human skin EST 234
c.497	7.8	45.9	11	1	ABV62390	Human skin EST 176
c 498	7.8	45.9	11	1	ABV68442	Human skin EST 622
499	7.8	45.9	11	1	ABV70691	Human skin EST 847
500	7.8	45.9	11	1	ABV63270	Human skin EST 105
c 501	7.8	45.9	11	1	ABV65285	Human skin EST 307
c 502	7.8	45.9	11	1	ABV71984	Human skin EST 977
c 503	7.8	45.9	11	1	ABV71546	Human skin EST 933
c 504	7.8	45.9	11	1	ABV64125	Human skin EST 191
505	7.8	45.9	11	1	ABV68490	Human skin EST 627
c 506	7.8	45.9	11	1	ABV69811	Human skin EST 759
507	7.8	45.9	11	1	ADQ29773	Rat VR1 exon 1a tr
c 508	7.8	45.9	11	1	ADQ35874	Human hair-bearing
c 509	7.8	45.9	11	1	ADQ36404	Human hair-bearing
510	7.8	45.9	11	1	ADQ33259	Human facial skin-
c 511	7.8	45.9	11	1	ADQ32561	Human facial skin-
c 512	7.8	45.9	11	1	ADQ33791	Human facial skin-
c 513	7.8	45.9	11	1	ADQ32382	Human facial skin-

ALIGNMENTS

RESULT 1
AAT89947
ID AAT89947 standard; DNA; 17 BP.
XX
AC AAT89947;
XX
DT 05-MAR-1998 (first entry)
XX
DE Human Interleukin-1 receptor antagonist intron 2 PCR primer 1.
XX
KW Interleukin-1 receptor antagonist; IL-1ra; ulcerative colitis; diagnosis;
KW prognosis; inflammatory bowel disease; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9725445-A1.
XX
PD 17-JUL-1997.
XX
PF 08-JAN-1997; 97WO-US000042.
XX
PR 12-JAN-1996; 96US-00587911.
XX
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
PA (UYVI-) UNIV VIRGINIA PATENT FOUND.

XX
PI Cominelli F, Pizarro T, Rotter JI, Yang H;
XX
DR WPI; 1997-372880/34.
XX
PT Screening for ulcerative colitis in subjects of Jewish ancestry - by
PT detecting allele 2 of the VNTR (variable number of tandem repeats)
PT polymorphism at intron 2 of the IL-1 receptor antagonist gene.
XX
PS Claim 7; Page 17; 22pp; English.
XX
CC This PCR primer and primer AAT89948 are used to amplify intron 2 of the
CC human interleukin-1 receptor antagonist gene (IL-1ra) in a novel method
CC to screen for ulcerative colitis (UC) in a subject of Jewish ancestry.
CC There is an association between allele 2 of the variable number of tandem
CC repeats (VNTR) polymorphism at intron 2 of IL-1ra, an important
CC endogenous regulator of inflammation, and UC in humans of Jewish
CC ancestry. This method can be used for the diagnosis and prognosis of UC
CC in Jewish patients for UC and distinguishing UC from Crohn's disease (CD)
CC and other inflammatory disease of the bowel
XX
SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
||||||||||||||||||
Db 1 CTCAGCAACACTCCTAT 17

RESULT 2
AAT89409
ID AAT89409 standard; cDNA; 17 BP.
XX
AC AAT89409;
XX
DT 22-APR-1998 (first entry)
XX
DE Human IL-1RN gene intron 2 PCR primer 1.
XX
KW Osteoporosis; interleukin-1 receptor antagonist; IL-1RN; allele;
KW bone mineral density; post-menopause; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9738135-A1.
XX
PD 16-OCT-1997.
XX
PF 03-APR-1997; 97WO-US005626.
XX
PR 05-APR-1996; 96US-00628282.
XX
PA (MEDI-) MEDICAL SCI SYSTEMS INC.
XX
PI Duff GW, Russell G, Eastell R;
XX
DR WPI; 1997-512741/47.
XX
PT Detecting genetic predisposition for osteoporosis - by detecting
PT interleukin-1 receptor antagonist gene IL-1RN allele 2 in the genomic DNA
PT of a patient.
XX
PS Claim 2; Page 9; 21pp; English.
XX
CC PCR primers AAT89409 and AAT89410 are used to amplify a region of the
CC interleukin-1 receptor antagonist gene, IL-1RN, intron 2 which contains a
CC variable number tandem repeat (VNTR) region that gives rise to five
CC alleles. This product is used for predicting the risk of osteoporosis in
CC a subject by determining the allelic and genetic polymorphism pattern for
CC IL-1RN in genomic DNA. A pattern of at least one copy of the IL-1RN
CC allele 2 indicates an increased susceptibility to osteoporosis. The
CC methods can predict low bone mineral density (BMD) and the rate of bone
CC density loss and thereby a susceptibility to osteoporosis. Individuals so
CC identified can then be treated more aggressively to prevent or retard the
CC occurrence of disease
XX
SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
||||||||||||||||||
Db 1 CTCAGCAACACTCCTAT 17

RESULT 3
AAV62390
ID AAV62390 standard; DNA; 17 BP.
XX
AC AAV62390;
XX
DT 19-JAN-1999 (first entry)
XX
DE IL-1 receptor antagonist gene intron 2 PCR primer #1.
XX
KW Human; interleukin-1 receptor antagonist gene; IL-1; polymorphism;
KW diagnosis; osteoporosis; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9844150-A1.
XX
PD 08-OCT-1998.
XX
PF 27-MAR-1998; 98WO-GB000944.
XX
PR 27-MAR-1997; 97GB-00006359.
XX
PA (GEMI-) GEMINI RES LTD.
XX
PI Keen RW, Spector TD;
XX
DR WPI; 1998-557135/47.
XX
PT Diagnosis of osteoporosis by determining genotype of interleukin-1
PT receptor antagonist gene - useful for diagnosing patient pre-disposition
PT or susceptibility to osteoporosis and for therapeutic intervention.
XX
PS Claim 9; Page 10; 36pp; English.
XX
CC A method has been developed for the diagnosis of osteoporosis comprising
CC determining the genotype of an interleukin-1 (IL-1) receptor antagonist
CC gene (IL-1RN). The present sequence represents a PCR primer adapted to
CC amplify a portion of intron 2 of an IL-1RN for use in the method of the
CC invention. The method can be used for the diagnosis of disease, including
CC diagnosis of osteoporosis and predisposition or susceptibility to
CC osteoporosis and for therapy
XX
SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
||||||||||||||||||
Db 1 CTCAGCAACACTCCTAT 17

```
RESULT 4
AAV60230
ID   AAV60230 standard; DNA; 17 BP.
XX
AC   AAV60230;
XX
DT   25-NOV-1998  (first entry)
XX
DE   PCR primer used to amplify interleukin-1 receptor antagonist (IL-1RN).
XX
KW   Interleukin-1 receptor antagonist; IL-1RN; predisposition;
KW   coronary artery disease; screen; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9840517-A1.
XX
PD   17-SEP-1998.
XX
PF   09-MAR-1998;   98WO-US004725.
XX
PR   10-MAR-1997;   97US-00813456.
XX
PA   (MEDI-) MEDICAL SCI SYSTEMS INC.
XX
PI   Francis SE,  Crossman DC,  Duff GW;
XX
DR   WPI; 1998-520829/44.
XX
PT   Detection of predisposition to coronary artery disease - by comparative
PT   measurement of levels of expression of alleles from the interleukin 1
PT   locus.
XX
PS   Claim 6; Page 15; 22pp; English.
XX
CC   PCR primers AAV60230-31 were used to amplify alleles associated with the
CC   interleukin-1 receptor antagonist (IL-1RN). The specification describes a
CC   method for determination of a patient's predisposition to coronary artery
CC   disease. The method comprises comparing an allele with a second allele
CC   which is predictive of coronary artery disease, where similarity between
CC   the first and second alleles indicates a predisposition to coronary
CC   artery disease. The method is used to genotype an individual's
CC   interleukin (IL)-1 loci, the overexpression of which correlates with
CC   coronary artery disease. The method is used to screen a patients'
CC   predisposition to coronary artery disease
XX
SQ   Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 5
AAV32393
ID   AAV32393 standard; DNA; 17 BP.
XX
AC   AAV32393;
XX
DT   11-SEP-1998  (first entry)
XX
DE   Interleukin-1RN primer 1.
XX
KW   Genetic polymorphism; PCR; primer; amplification; interleukin-1RN;
KW   sight threatening diabetic retinopathy; interleukin-1-alpha; IL-1RN;
KW   interleukin-1-beta; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9815653-A1.
XX
PD   16-APR-1998.
XX
PF   09-OCT-1997;   97WO-GB002790.
XX
PR   10-OCT-1996;   96GB-00021129.
XX
PA   (DUFF/) DUFF G.
PA   (RENN/) RENNIE I.
PA   (RICH/) RICHARDSON R.
XX
PI   Duff G,  Rennie I,  Richardson R;
XX
DR   WPI; 1998-240835/21.
XX
PT   Predicting increased risk of sight-threatening diabetic retinopathy -
PT   comprises identifying genetic polymorphism pattern for genes IL-1A, IL-1B
PT   and IL-1RN, useful to allow treatment before clinical symptoms occur.
XX
PS   Claim 2; Page 33; 41pp; English.
XX
CC   Interleukin-1RN (IL-1RN) primers 1 and 2 (AAV32394) were used to amplify
CC   the IL-1RN gene region to identify polymorphism of the VNTR region at the
CC   IL-1RN intron 2 locus. The invention claims to provide a method for
CC   predicting the risk of sight threatening diabetic retinopathy. The method
CC   involves isolating DNA from a patient and determining the DNA
CC   polymorphism pattern of the genes that code for interleukin-1-alpha,
CC   interleukin-1-beta and interleukin-1RN. The polymorphic pattern
CC   identified is then compared with controls of known DNA polymorphism
CC   patterns thereby identifying patients carrying a genetic polymorphism
CC   associated with increased risk of sight threatening diabetic retinopathy.
CC   The method may be able to identify diabetic patients at risk before the
CC   clinically detectable disorders occur. Polymorphism pattern determination
CC   of IL genes involved PCR reactions using primers AAV32389-V32398. The
CC   method is also claimed to be useful in conjunction with identification of
CC   other genes associated with sight threatening diabetic retinopathy in
CC   genomic DNA and therefore, in identifying diabetic patients expressing
CC   multiple risk patterns
XX
SQ   Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 6
AAZ10706
ID   AAZ10706 standard; DNA; 17 BP.
XX
AC   AAZ10706;
XX
DT   23-NOV-1999  (first entry)
XX
DE   PCR primer 1 used to amplify part of the interleukin-IRN gene.
XX
KW   Polymorphism; interleukin-IRN; IL-IRN; chronic ulcer;
KW   inflammatory cytokine; dermal ulcer; venous ulcer; pressure sore;
KW   decubitis ulcer; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   GB2336431-A.
XX
PD   20-OCT-1999.
XX
```

PF 17-APR-1998; 98GB-00008202.
XX
PR 17-APR-1998; 98GB-00008202.
XX
PA (JOHJ) JOHNSON & JOHNSON MEDICAL LTD.
XX
PI Harvey W;
XX
DR WPI; 1999-543555/46.
XX
PT Polymorphism typing for genes encoding inflammatory cytokines useful for
PT the analysis of chronic ulcers.
XX
PS Example; Page 19; 25pp; English.
XX
CC PCR primers AAZ10706-07 were used to identify a polymorphism in intron 2
CC of the interleukin-IRN (IL-IRN) gene, in the method of the invention. The
CC specification describes a method for diagnosing the susceptibility to
CC chronic ulcers, predicting their severity and/or the efficacy of the
CC healing response generated by the body comprises polymorphism typing for
CC genes encoding inflammatory cytokines. The method can be used for the
CC analysis of dermal ulcers e.g. venous ulcers, pressure sores or decubitis
CC ulcers. The analysis can be used to provide an early diagnosis of the
CC predisposition to developing a chronic ulcer. Patients can be supervised
CC over a period of time at which they are thought to be at risk from
CC developing a chronic ulcer to allow early diagnosis and preventative
CC intervention before the clinical symptoms are noticed. Individual
CC treatments can then be used to suit patients with subtle differences in
CC their disease state
XX
SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
||||||||||||||||||
Db 1 CTCAGCAACACTCCTAT 17

RESULT 7
AAX75917
ID AAX75917 standard; DNA; 17 BP.
XX
AC AAX75917;
XX
DT 29-JUL-1999 (first entry)
XX
DE Human interleukin 1 PCR primer SEQ ID NO:5.
XX
KW Human; interleukin 1; IL-1B; IL-1A; IL-1RN; diagnosis; detection;
KW chronic obstructive airway disease; chronic bronchitis; emphysema;
KW asthma; chronic bronchiolitis; proinflammatory haplotype; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9924615-A2.
XX
PD 20-MAY-1999.
XX
PF 09-NOV-1998; 98WO-US023721.
XX
PR 07-NOV-1997; 97GB-00023553.
PR 12-JAN-1998; 98US-00005923.
XX
PA (MEDI-) MEDICAL SCI SYSTEMS INC.
XX
PI Duff GW, Giovine M, Barnes PJ, Lim S;
XX
DR WPI; 1999-327420/27.
XX
PT Genotyping nucleic acid samples for interleukin-1 (IL-1) proinflammatory
PT haplotype alleles, useful for predicting susceptibility to developing
PT chronic obstructive airway disease.
XX
PS Claim 7; Page 20; 37pp; English.
XX
CC The present invention describes genotyping a nucleic acid sample from a
CC subject to determine at least one allele of an interleukin-1 (IL-1)
CC proinflammatory haplotype. A method has also bee described for
CC determining a subject's susceptibility to developing chronic obstructive
CC airway disease (COAD) or for predicting the rapidity or ultimate
CC progression of a COAD in the subject by: (a) obtaining a nucleic acid
CC sample from the subject; and (b) detecting at least one allele of an IL-1
CC proinflammatory haplotype in the sample, where detection of at least one
CC of these alleles indicates that the patient has an increased
CC susceptibility to developing COAD. The method is useful for determining
CC the susceptibility of subjects to developing chronic obstructive airway
CC disease or for predicting the rapidity or ultimate progression of chronic
CC obstructive airway disease (COAD). COAD can be asthma, emphysema, chronic
CC bronchitis or chronic bronchiolitis. The method provides for early
CC identification of chronic obstructive airway disease (COAD), facilitating
CC administration of appropriate treatment at the earliest stage, thereby
CC increasing the probability of a positive outcome. The present sequence
CC represents a PCR primer used in the method of the invention
XX
SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
||||||||||||||||||
Db 1 CTCAGCAACACTCCTAT 17

RESULT 8
AAX16621
ID AAX16621 standard; DNA; 17 BP.
XX
AC AAX16621;
XX
DT 29-APR-1999 (first entry)
XX
DE Interleukin 1 (44112332) haplotype PCR primer #15.
XX
KW Interleukin 1; IL-1; haplotype; inflammatory disorder; alopecia areata;
KW coronary artery disease; osteoporosis; nephropathy; diabetes mellitus;
KW Graves disease; systemic lupus erythamatosus; lichen sclerosis;
KW ulcerative colitis; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9854359-A1.
XX
PD 03-DEC-1998.
XX
PF 21-MAY-1998; 98WO-GB001481.
XX
PR 29-MAY-1997; 97GB-00011040.
XX
PA (DUFF/) DUFF G.
PA (COXA/) COX A.
PA (CAMP/) CAMP N J.
PA (DGIO/) DE GIOVINE F S.
XX
PI Duff G, Cox A, Camp NJ, De Giovine FS;
XX
DR WPI; 1999-080814/07.
XX
PT New method of determining a patient's susceptibility to inflammatory
PT disorders - by detecting the presence of an IL-1 (44112332) haplotype,

```
PT   useful in designing treatment strategies that modulate the activity of
PT   proteins produced by the IL-1 gene cluster.
XX
PS   Claim 3; Page 33; 49pp; English.
XX
CC   A method has been developed for determining a patient's susceptibility to
CC   an inflammatory disorder. The method comprises the detection of an
CC   interleukin 1 (IL-1) (44112332) haplotype in a sample obtained from the
CC   patient, where its presence indicates susceptibility to an inflammatory
CC   disorder. AAX16607 to AAX16631 represent PCR primer used in the method
CC   for detecting the IL-1 (44112332) haplotype. The method provides kits for
CC   the early prediction of a patient's susceptibility to inflammatory
CC   disorders, including coronary artery disease, osteoporosis, nephropathy
CC   in diabetes mellitus, alopecia areata, Graves disease, systemic lupus
CC   erythamatosus, lichen sclerosis and ulcerative colitis. The detection of
CC   alleles of the haplotype can be applied to particular inflammatory
CC   disorders, comprising diabetic retinopathy, juvenile chronic arthritis,
CC   psoriasis, and insulin dependent diabetes. The identification of a
CC   disease-associated haplotype enables determination of which alleles are
CC   causative, and this information is useful in designing treatment
CC   strategies, including gene therapy and treatment using various agents
CC   that modulate the activity of proteins produced by the IL-1 gene cluster.
CC   Some alleles from the IL-1 gene cluster are associated with particular
CC   inflammatory diseases, and insufficient IL-1 production appears to act
CC   centrally in the pathology of these diseases. Therefore, the use of IL-1
CC   gene clusters is useful in determining genetic susceptibility to
CC   inflammatory diseases, including those with a multifactorial etiology
CC   with a polygenic component
XX
SQ   Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
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Db          1 CTCAGCAACACTCCTAT 17


RESULT 9
ABX15549
ID   ABX15549 standard; DNA; 17 BP.
XX
AC   ABX15549;
XX
DT   11-APR-2003  (first entry)
XX
DE   Human IL-1 genotyping marker VNTR primer #1.
XX
KW   Human; ss; PCR; primer; interleukin-1; IL-1; marker VNTR; nephropathy;
KW   inflammatory disease; Systemic Inflammatory Response; SIRS; genotyping;
KW   Alzheimer's disease; arthritis; acute joint inflammation; opthalmopathy;
KW   juvenile chronic arthritis; asthma; bronchial asthma; pulmonary disease;
KW   chronic obstructive airways disease; cardiovascular disease; thyroditis;
KW   atherosclerosis; autoimmune carditis; cardiomyopathy; ulcerative colitis;
KW   cardiac cell disfunction; aortic smooth muscle cell activation; trauma;
KW   cardiac cell apoptosis; gastrointestinal inflammation; cerebral trauma;
KW   inflammatory bowel disease; HIV infection; coronary artery lesion;
KW   Kawasaki's syndrome; cervical lymphadenopathy; diabetic nephropathy;
KW   glomerulonephritis; diabetic retinopathy; Grave's opthalmopathy;
KW   osteoporosis; bone loss; otitis media; pancreatitis; periodontal disease;
KW   chronic lung disease; chronic sinusitis; chronic lymphocytic thyroditis;
KW   urinary tract infection; chronic prostatitis; immunological disorder;
KW   chronic pelvic pain syndrome; alopecia areata; Grave's disease;
KW   thyroid disease; goiter; struma lymphomatosa; sleep disorder; neoplasia;
KW   chronic fatigue syndrome; obesity; infectious disease; Leishmaniasis;
KW   Leprosy; myocardial disfunction; breast cancer; organ transplant;
KW   Hodgkin's disease; hormonal regulation; fertility; septicaemia.
XX
OS   Homo sapiens.
XX
PN   US2002146700-A1.
XX
PD   10-OCT-2002.
XX
PF   27-APR-2001; 2001US-00845129.
XX
PR   29-MAY-1997;   97GB-00011040.
PR   30-JUN-1999;   99US-00345217.
XX
PA   (INTE-) INTERLEUKIN GENETICS INC.
XX
PI   Duff GW,  Cox A,  Camp NJ,  Di Giovine FS;
XX
DR   WPI; 1999-080814/07.
XX
PT   New method of determining a patient's susceptibility to inflammatory
PT   disorders - by detecting the presence of an IL-1 (44112332) haplotype,
PT   useful in designing treatment strategies that modulate the activity of
PT   proteins produced by the IL-1 gene cluster.
XX
PS   Claim 5; Page 20; 42pp; English.
XX
CC   The invention relates to a method for determining whether a subject has
CC   or is predisposed to developing a disease or condition that is associated
CC   with an IL-1 inflammatory haplotype. The method involves detecting at
CC   least one allele of the haplotype, where the presence of the allele
CC   indicates that the subject is predisposed to the development or has the
CC   disease or condition. The invention allows the determination of an
CC   individual's likelihood for developing a particular disease or condition
CC   associated with interleukin 1 (IL-1) polymorphisms without necessarily
CC   determining or characterising the causative genetic variation. Diseases
CC   such as inflammatory disease e.g. Systemic Inflammatory Response (SIRS),
CC   Alzheimer's disease; arthritis e.g. acute joint inflammation, juvenile
CC   chronic arthritis; asthma e.g. bronchial asthma, chronic obstructive
CC   airways disease; cardiovascular diseases e.g atherosclerosis, autoimmune
CC   carditis; cardiomyopathy and cardiac cell disfunction e.g. aortic smooth
CC   muscle cell activation, cardiac cell apoptosis; gastrointestinal
CC   inflammations e.g. inflammatory bowel disease, ulcerative colitis; HIV
CC   infection; Kawasaki's syndrome e.g. cervical lymphadenopathy, coronary
CC   artery lesions; nephropathies e.g. diabetic nephropathy,
CC   glomerulonephritis; opthalmopathies e.g. diabetic retinopathy, Grave's
CC   opthalmopathy; osteoporosis e.g. bone loss, otitis media; pancreatitis;
CC   periodontal disease; pulmonary diseases e.g. chronic lung disease,
CC   chronic sinusitis; thyroditis e.g. chronic lymphocytic thyroditis;
CC   urinary tract infections e.g. chronic prostatitis, chronic pelvic pain
CC   syndrome; immunological disorders e.g. alopecia areata, Graves disease;
CC   thyroid diseases e.g. goiter, struma lymphomatosa; sleep disorders;
CC   chronic fatigue syndrome; obesity; infectious diseases e.g. Leprosy,
CC   Leishmaniasis; trauma e.g. cerebral trauma, myocardial disfunction;
CC   neoplasias e.g breast cancer, Hodgkin's disease; hormonal regulation e.g.
CC   fertility, septicaemia; organ transplants. This allows for a more
CC   customised approach to preventing the onset or progression of the disease
CC   or condition, e.g. a clinician can more effectively prescribe a therapy
CC   that will address the molecular basis of the disease or condition. The
CC   present sequence represents the sequence of the human IL-1 genotyping
CC   marker VNTR primer #1
XX
SQ   Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 10
AAZ37216
ID   AAZ37216 standard; DNA; 17 BP.
XX
AC   AAZ37216;
XX
```

DT 28-JAN-2000 (first entry)
XX
DE PCR primer for interleukin-1RN (VNTR).
XX
KW PCR primer; IL-1; IL-1A; IL-1B; TNFA; interleukin-1; foetus;
KW adverse pregnancy outcome; allele detection; low birth weight; LBW;
KW pre-term baby; premature baby; tumour necrosis factor-alpha; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9954707-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-US008794.
XX
PR 21-APR-1998; 98US-0082487P.
XX
PA (MEDI-) MEDICAL SCI SYSTEMS INC.
XX
PI Kornman KS, Offenbacher S, Duff GW;
XX
DR WPI; 2000-013279/01.
XX
PT Fetal testing for prediction of low birth weight by detecting an
PT interleukin allele.
XX
PS Claim 5; Page 73; 78pp; English.
XX
CC This sequence represents a PCR primer for interleukin-1RN (IL-1RN). The
CC invention relates to a method for determining whether a foetus is
CC predisposed to having an adverse pregnancy outcome by detecting an
CC interleukin-1A (IL-1A) (+4845) allele 2, an IL-1 (-511) allele 1 or an
CC allele in linkage disequilibrium with either of these alleles. The method
CC comprises: (a) obtaining a nucleic acid sample from the subject; and (b)
CC detecting an IL-1A (+4845) allele 2, an IL-1 (-511) allele 1 or an allele
CC in linkage disequilibrium with either of these alleles, where detection
CC of the alleles or an allele in linkage disequilibrium with them indicates
CC that the fetus is predisposed to an adverse pregnancy outcome. The method
CC is used to determine whether a fetus is predisposed to having a low birth
CC weight (LBW). By determining the IL-1 or tumour necrosis factor-alpha
CC (TNF-A) genotype an appropriate therapeutic, such as a corticosteroid,
CC antimetabolite, cytotoxic drug, colchicine or anti-cytokine, can be
CC administered to compensate for the LBW causative functional mutation. An
CC appropriate therapeutic can be used to treat a subject predisposed to
CC having a LBW baby, especially a pre-term or premature baby
XX
SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
||||||||||||||||||
Db 1 CTCAGCAACACTCCTAT 17

RESULT 11
AAA61915
ID AAA61915 standard; DNA; 17 BP.
XX
AC AAA61915;
XX
DT 20-NOV-2000 (first entry)
XX
DE Human IL-1RN (VNTR) polymorphic locus PCR primer, SEQ ID NO:1.
XX
KW Human; IL-1 gene cluster; interleukin-1; chromosome 2q13-14;
KW proinflammatory; cytokine; systemic inflammatory response; sepsis;
KW dyregulation; pattern 2 allele; genotyping; IL-1RN gene;
KW IL-1 receptor antagonist; IL-1RN (VNTR) polymorphic locus;
KW variable number of tandem repeats; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200037679-A2.
XX
PD 29-JUN-2000.
XX
PF 01-NOV-1999; 99WO-US025633.
XX
PR 30-OCT-1998; 98US-00183850.
XX
PA (INTE-) INTERLEUKIN GENETICS INC.
XX
PI Di Giovine FS, Duff GW;
XX
DR WPI; 2000-442691/38.
XX
PT Determining susceptibility to developing sepsis for preventing or
PT treating sepsis, involves detecting an allele of interleukin-1 genetic
PT pattern that leads to disregulated inflammatory response.
XX
PS Disclosure; Page 35; 66pp; English.
XX
CC The invention relates to methods of determining an individual's
CC susceptibility to developing and/or rapidly progressing into sepsis via
CC genotyping of a member of the IL-1 (interleukin-1) gene cluster. The
CC method comprises obtaining an IL-1 gene cluster nucleic acid from an
CC individual and determining whether that individual's DNA contains at
CC least one allele of an IL-1 genetic pattern that leads to a dysregulated
CC inflammatory response. The presence of a pattern 2 allele or a marker in
CC linkage disequilibrium with a pattern 2 allele in the sample, indicates
CC that the patient has an increased susceptibility to developing sepsis.
CC The IL-1 gene cluster comprises a region of 430 kb which is located on
CC the long arm of chromosome 2 (2q13-14). It contains the IL-1A gene which
CC encodes IL-1-alpha, the IL-1B gene which encodes IL-1-beta, and the IL-
CC 1RN gene which encodes the IL-1 receptor antagonist. IL-1 is a
CC proinflammatory cytokine released by macrophages which can induce a
CC systemic response to local injury or infection. It thus plays a key role
CC in the development of sepsis, which can lead to intravascular
CC coagulation, multiple organ failure, cardiovascular collapse, and death.
CC It is therefore useful to identify those individuals who are at risk of
CC developing an exaggerated systemic inflammatory response to septic
CC stimuli, so that sepsis therapy (e.g, with IL-1 modulators) can be
CC tailored to the individual's genetic profile. Sequences AAA61915-A61928
CC represent PCR primers which may be used to amplify IL-1 gene cluster
CC polymorphic loci. Sequences AAA61915-A61916 are primers used to amplify
CC and type the IL-1RN (VNTR) (variable number of tandem repeats)
CC polymorphic locus
XX
SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
||||||||||||||||||
Db 1 CTCAGCAACACTCCTAT 17

RESULT 12
AAC63787
ID AAC63787 standard; DNA; 17 BP.
XX
AC AAC63787;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human IL-1RN gene VNTR primer #1.
XX
KW Human; IL-1RN; interleukin-1 receptor; cytostatic; antiinflammatory;
KW immunosuppressive; dermatological; antimicrobial; antiarthritic;

KW IL-1 receptor antagonist;
KW tumour necrosis factor alpha antagonist interstitial lung disease;
KW interstitial pneumonia; pulmonary fibrosis; rheumatoid arthritis;
KW systemic lupus erythmatosis; Sjogren's syndrome; systemic sclerosis;
KW dermatomyocitis; chromosome 2; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200060117-A2.
XX
PD 12-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US008492.
XX
PR 02-APR-1999; 99US-00286108.
XX
PA (INTE-) INTERLEUKIN GENETICS INC.
XX
PI Duff GW, Di Giovine FS, Whyte M;
XX
DR WPI; 2000-656234/63.
XX
PT Method for predicting the risk of interstitial lung disease, comprising
PT detecting an interleukin-1 receptor antagonist allele and tumor necrosis
PT alpha allele or an allele in linkage disequilibrium with either of these
PT alleles.
XX
PS Example 2; Page 72; 102pp; English.
XX
CC The present sequence is provided in a specification relating to a method
CC for determining whether a subject has or is predisposed to develop an
CC interstitial lung disease. The method involves detecting an interleukin-1
CC receptor antagonist (IL-1RN) (+2018) allele 2, a tumour necrosis alpha
CC (TNF-A)(-308) allele 2, or an allele in linkage disequilibrium with
CC either of these two alleles. The method may be used to determine whether
CC a subject has or is predisposed to develop an interstitial pneumonia or a
CC pulmonary fibrosis and other disorders such as rheumatoid arthritis,
CC systemic lupus erythmatosis, Sjogren's syndrome, systemic sclerosis,
CC dermatomyocitis. The method is also used for identifying molecules which
CC can be used as therapeutics for treating interstitial lung disease
XX
SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
||||||||||||||||||
Db 1 CTCAGCAACACTCCTAT 17

RESULT 13
AAF27686
ID AAF27686 standard; DNA; 17 BP.
XX
AC AAF27686;
XX
DT 02-APR-2001 (first entry)
XX
DE Primer #19.
XX
KW IL-1; interleukin; inflammation; infection; ss.
XX
OS Unidentified.
XX
PN WO200100880-A2.
XX
PD 04-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US018318.
XX
PR 30-JUN-1999; 99US-00345217.
XX
PA (INTE-) INTERLEUKIN GENETICS INC.
XX
PI Duff GW, Cox A, Camp NJ, Di Giovine FS;
XX
DR WPI; 2001-102903/11.
XX
PT Determining whether a subject has or is predisposed to disease associated
PT with IL-1 polymorphism involves determining presence of marker or allele
PT comprising IL-1 inflammatory haplotype.
XX
PS Claim 5; Page 48; 84pp; English.
XX
CC The present invention relates to a new method for determining whether a
CC subject has or is predisposed to developing a disease or condition that
CC is associated with an IL (interleukin)-1 inflammatory haplotype,
CC comprises detecting at least one allele of the haplotype, where the
CC presence of the allele indicates that the subject is predisposed to the
CC development or has the disease or condition. The method is useful for
CC determining whether a subject has or is predisposed to inflammatory
CC disease, a degenerative disease, an immunological disorder, an infectious
CC disease, trauma induced disease, or cancer. The above conditions
CC associated with an IL-1 inflammatory haplotype can be treated or
CC prevented by administering a therapeutic that compensates for a causative
CC mutation that is in linkage disequilibrium with at least one IL-1
CC polymorphism
XX
SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
||||||||||||||||||
Db 1 CTCAGCAACACTCCTAT 17

RESULT 14
AAC89171
ID AAC89171 standard; DNA; 17 BP.
XX
AC AAC89171;
XX
DT 08-MAR-2001 (first entry)
XX
DE Human IL-1RN (VNTR) polymorphic locus PCR primer #1.
XX
KW Human; PCR primer; cardiant; vasotropic; polymorphic; chromosome 2q13;
KW interleukin-1 gene cluster; IL-1; cardiovascular disorder; IL-1RN;
KW fragile plaque disorder; occlusive disorder; in-stent restenosis; ss.
XX
OS Homo sapiens.
XX
PN WO200072015-A2.
XX
PD 30-NOV-2000.
XX
PF 26-MAY-2000; 2000WO-US014775.
XX
PR 26-MAY-1999; 99US-00320395.
PR 01-NOV-1999; 99US-00431352.
XX
PA (INTE-) INTERLEUKIN GENETICS INC.
XX
PI Francis SE, Crossman DC, Duff GW, Kornman KS;
XX
DR WPI; 2001-032066/04.
XX
PT Diagnosing cardiovascular disease, or susceptibility, useful e.g. for
PT selecting treatment, from presence of disease-associated allele,
PT particularly in interleukin-1 genes.
XX

PS Claim 11; Page 79; 121pp; English.
XX
CC There is an association of patterns of alleles at four polymorphic loci
CC in the interleukin-1 (IL-1) gene cluster with cardiovascular disorders.
CC The present invention relates to a method for the diagnosis of a
CC cardiovascular disorder (CVD), via detecting a CVD-associated allele in a
CC patient sample. The method is used to select an appropriate therapy for
CC CVD, particularly fragile plaque disorder, occlusive disorders or in-
CC stent restenosis, or a condition associated with a mutation with linkage
CC disequilibrium with a CVD-associated allele, or to identify risk factors
CC for CVD, and to formulate a treatment designed to reduce the risk. The
CC present sequence is a PCR primer used in the present invention. The IL-1
CC gene cluster is found at the 2q13 region of chromosome 2
XX
SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
||||||||||||||||||
Db 1 CTCAGCAACACTCCTAT 17

RESULT 15
AAC91425
ID AAC91425 standard; DNA; 17 BP.
XX
AC AAC91425;
XX
DT 20-MAR-2001 (first entry)
XX
DE Human IL-1RN (VNTR) polymorphic locus 5' PCR primer.
XX
KW Human; IL-1A; interleukin-1alpha; IL-1B; interleukin-1beta; IL-1RN;
KW interleukin-1 receptor antagonist; vasotropic; antiinflammatory;
KW hypotensive; anticoagulant; antilipaemic; arterial restenosis;
KW restenosis associated allele; RAA; occlusive cardiovascular disorder;
KW restenosis detection; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200071753-A2.
XX
PD 30-NOV-2000.
XX
PF 24-MAY-2000; 2000WO-US014299.
XX
PR 24-MAY-1999; 99US-00317674.
PR 01-NOV-1999; 99US-00431352.
XX
PA (INTE-) INTERLEUKIN GENETICS INC.
XX
PI Kornman KS, Duff GW, Crossman DC, Francis SE, Stephenson K;
XX
DR WPI; 2001-025173/03.
XX
PT Diagnosing or determining susceptibility to developing restenosis
PT involves detecting restenosis associated allele in a nucleic acid sample.
XX
PS Claim 5; Page 11; 129pp; English.
XX
CC The present sequence may be used in a method for determining whether a
CC subject has or is predisposed to developing an arterial restenosis. The
CC method comprises detecting a restenosis associated allele (RAA) in a
CC nucleic acid sample from the subject, where detection of the RAA
CC indicates that the subject has or is predisposed to the development of a
CC restenosis. The restenosis associated allelic pattern permits the
CC diagnosis of occlusive cardiovascular disorder. The diagnosis allows the
CC most suitable treatment methods for restenosis to be used e.g. selecting
CC therapies for initial vascular stenosis most likely to avoid subsequent
CC stenoses. The detection methods identify restenosis therapeutics,
CC agonists and antagonists, (proteins, peptides, peptidomimetics, small
CC molecules or nucleic acids, e.g. anti-sense, ribozyme and triplex nucleic
CC acids) which are used to treat restenosis
XX
SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
||||||||||||||||||
Db 1 CTCAGCAACACTCCTAT 17

RESULT 16
AAD27377
ID AAD27377 standard; DNA; 17 BP.
XX
AC AAD27377;
XX
DT 18-APR-2002 (first entry)
XX
DE PCR primer #1, used for genotyping human IL-1RN (VNTR) marker.
XX
KW Human; interleukin-1; inflammatory disorder; coronary artery disease;
KW periodontal disease; Alzheimer's disease; atherosclerosis; osteoporosis;
KW immune response; insulin-dependent diabetes; diabetic retinopathy;
KW renal disease; diabetic nephropathy; hepatic fibrosis; alopecia areata;
KW Graves disease; Graves ophthalmopathy; systemic lupus erythematosus;
KW extrathyroid disease; lichen sclerosis; juvenile chronic arthritis;
KW rheumatoid arthritis; gastric cancer; ulcerative colitis; asthma;
KW interstitial lung disease; idiopathic pulmonary fibrosis; sepsis;
KW multiple sclerosis; acne; IL-1 receptor antagonist; IL-1RN; VNTR;
KW cardiant; dermatological; nootropic; neuroprotective; osteopathic;
KW ophthalmological; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200200933-A2.
XX
PD 03-JAN-2002.
XX
PF 22-JUN-2001; 2001WO-US020079.
XX
PR 23-JUN-2000; 2000US-0213853P.
XX
PA (INTE-) INTERLEUKIN GENETICS INC.
XX
PI Duff GW, Kornman KS;
XX
DR WPI; 2002-139934/18.
XX
PT Screening a substance in a subject for modulating an immune response,
PT comprises genotyping to identify the test subject, and observing a
PT biomarker before and after contacting the subject with the test
PT substance.
XX
PS Example; Page 40; 54pp; English.
XX
CC The present invention relates to methods for identifying a test substance
CC that modulate the immune response in a genotype specific manner. Methods
CC of the invention involve genotyping subjects to identify those having a
CC genotype (e.g. interleukin-1; IL-1) associated with one or more
CC inflammatory disorder. The method comprises genotyping a subject having
CC an inflammatory disease-associated genotype and observing a biomarker in
CC the subject before and after the subject is contacted with the test
CC substance. The methods or cells associated with inflammatory diseases are
CC useful for identifying a substance that is likely to prevent or diminish
CC a specific biological response in subjects having inflammatory disease-
CC associated genotype, where the genotype is associated a pre- disposition
CC to one or more of periodontal disease, coronary artery disease,
CC Alzheimer's disease, atherosclerosis, osteoporosis, insulin- dependent

```
CC   diabetes, diabetic retinopathy, end-stage renal disease, diabetic
CC   nephropathy, hepatic fibrosis, alopecia areata, Graves disease, Graves
CC   ophthalmopathy, extrathyroid disease, systemic lupus erythematosus,
CC   lichen sclerosis, rheumatoid arthritis, juvenile chronic arthritis,
CC   gastric cancer, ulcerative colitis, asthma, interstitial lung disease,
CC   multiple sclerosis, idiopathic pulmonary fibrosis, sepsis and acne. The
CC   invention also relates to a kit comprising primers for the identification
CC   of one or more IL-1 polymorphism. The present sequence is a PCR primer
CC   which is used for amplifying IL-1 receptor antagonist (IL-1RN; VNTR)
CC   gene. This primer is used in the exemplification of the invention for
CC   genotyping IL-1RN marker
XX
SQ   Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 17
AAL54501
ID   AAL54501 standard; DNA; 17 BP.
XX
AC   AAL54501;
XX
DT   16-APR-2003  (first entry)
XX
DE   Ageing-related condition detection PCR primer, SEQ ID No 7.
XX
KW   Early onset; progression; ageing-related condition; EOA; allele;
KW   interleukin; (IL)-1; pattern 1; pattern 2; pattern 3; osteoporosis;
KW   osteoarthritis; wrinkled skin; age-related cancer; lifestyle; exercise;
KW   diet; nutraceutical; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   WO2002103031-A2.
XX
PD   27-DEC-2002.
XX
PF   17-JUN-2002; 2002WO-US019205.
XX
PR   15-JUN-2001; 2001US-0298493P.
XX
PA   (INTE-) INTERLEUKIN GENETICS INC.
XX
PI   Barnett K,  Crossman DC,  Duff GW,  Francis SE,  Kornman KS;
XX
DR   WPI; 2003-167530/16.
XX
PT   Determining a subject's susceptibility to an early onset or progression
PT   of an aging-related condition, useful for customizing therapy, comprises
PT   detecting the presence of an allele of an interleukin-1 pattern 1,
PT   pattern 2 and/or pattern 3.
XX
PS   Example 3; Page 52; 98pp; English.
XX
CC   The invention relates to a novel method for determining a subject's
CC   susceptibility to the early onset or progression of an ageing-related
CC   condition (EOA). The novel method comprises assessing the subject's
CC   genotype with respect to at least one allele of an interleukin (IL)-1
CC   pattern 1, pattern 2 and/or pattern 3 (the presence or absence of at
CC   least 1 allele provides information about the subject's susceptibility to
CC   an early onset or progression of an ageing-related condition). The method
CC   is useful for determining or predicting a subject's susceptibility to the
CC   early onset or progression of an ageing-related condition (e.g.
CC   osteoporosis, osteoarthritis, wrinkled skin, or age-related cancer) and
CC   for determining an ageing-related phenotype. The method may be a
CC   customised therapy based on the individual's genetic profile, to tailor a
CC   recommended lifestyle, including changes in exercise and diet, and to
CC   recommend nutraceuticals that are predicted to benefit a subject having a
CC   particular IL-1 genotype and EOA predisposition. This polynucleotide
CC   sequence represents a PCR primer used in the detection method for
CC   determining EOA predisposition of the invention
XX
SQ   Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 18
AAD51455
ID   AAD51455 standard; DNA; 17 BP.
XX
AC   AAD51455;
XX
DT   16-APR-2003  (first entry)
XX
DE   Human interleukin-1 (IL-1) gene amplifying PCR primer #7.
XX
KW   Drug screening; fungicide; gene therapy; antibacterial; infection;
KW   virucide; human; interleukin-1; IL-1; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO2002101015-A2.
XX
PD   19-DEC-2002.
XX
PF   11-JUN-2002; 2002WO-US018346.
XX
PR   11-JUN-2001; 2001US-0297305P.
XX
PA   (INTE-) INTERLEUKIN GENETICS INC.
XX
PI   Dower S,  Duff GW;
XX
DR   WPI; 2003-148793/14.
XX
PT   New detection reagent, useful for monitoring molecular assembly events to
PT   permit the dissection of genetic and non-genetic influences on biological
PT   activity, comprises an interactive sensor pair.
XX
PS   Disclosure; Page 41; 56pp; English.
XX
CC   The invention relates to methods, compositions and apparatus for
CC   monitoring molecular assembly events. It also relates to a detection
CC   reagent comprising an interactive sensor pair. The detection reagent is
CC   useful for monitoring molecular assembly events to permit the dissection
CC   of genetic and non-genetic influences on a particular biological
CC   activity. The method is useful for linking genetic variations to
CC   molecular and physiological events, drug screening, diagnostics, therapy
CC   selection and dosing, patient monitoring or environmental safety. The
CC   interactive sensor pairs may be used to screen for and identify novel
CC   agonists and antagonists or other molecules that modulate a biological
CC   activity. The method is also useful for selecting an appropriate targeted
CC   therapeutic for a subject having an infection, including viral, bacterial
CC   or fungal infection. It is also used in gene therapy. The present
CC   sequence is a PCR primer used for amplifying human interleukin-1 (IL-1)
CC   gene. This sequence is used to illustrate the method of the invention
XX
SQ   Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 19
ADL83329
ID   ADL83329 standard; DNA; 17 BP.
XX
AC   ADL83329;
XX
DT   01-JUL-2004  (first entry)
XX
DE   PCR primer #1for human IL-1RN (VNTR) DNA.
XX
KW   Single vessel coronary artery disease; SVD; restenosis;
KW   interleukin-1 receptor antagonist; IL-1RN; VNTR; allele; human; PCR;
KW   primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6720141-B1.
XX
PD   13-APR-2004.
XX
PF   24-MAY-2000; 2000US-00578534.
XX
PR   01-NOV-1999;   99US-00431352.
XX
PA   (INTE-) INTERLEUKIN GENETICS INC.
XX
PI   Crossman DC,  Duff GW,  Francis SE,  Kornman KS,  Stephenson K;
XX
DR   WPI; 2004-313649/29.
XX
PT   Determining whether a single vessel coronary artery disease (SVD) subject
PT   has or is predisposed to developing restenosis comprises detecting IL-1RN
PT   (VNTR) allele 1 or 2 in a nucleic acid sample from the subject.
XX
PS   Claim 4; SEQ ID NO 7; 76pp; English.
XX
CC   The present invention relates to a method for determining whether a
CC   single vessel coronary artery disease (SVD) subject has or is predisposed
CC   to developing restenosis. The method comprises detecting interleukin-1
CC   receptor antagonist (IL-1RN) (VNTR) allele 1 or 2 in a nucleic acid
CC   sample from the subject, where detection of IL-1RN (VNTR) allele 1 or 2
CC   indicates that the subject has or is predisposed to the development of
CC   restenosis. Also disclosed is a kit for performing the method above. In
CC   the method, the detecting step is selected from allele specific
CC   oligonucleotide (ASO) hybridisation, size analysis, sequencing,
CC   hybridisation, 5' nuclease digestion, single-stranded conformational
CC   polymorphism (SSCP), allele specific hybridisation, primer specific
CC   extension or oligonucleotide ligation assay. The method is useful for
CC   determining whether a single vessel coronary artery disease (SVD) subject
CC   has or is predisposed to developing restenosis. The present sequence
CC   represents a PCR primer used in the method of the invention.
XX
SQ   Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 20
ADN48846
ID   ADN48846 standard; DNA; 17 BP.
XX
AC   ADN48846;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Human secreted interleukin-1RN (IL-1RN) amplifying PCR primer #1.
XX
KW   Early-onset menopause; EOM; diagnosis; therapy; human; interleukin-1RN;
KW   IL-1RN; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6730476-B1.
XX
PD   04-MAY-2004.
XX
PF   04-AUG-2000; 2000US-00632657.
XX
PR   30-JUN-1999;   99US-00345217.
XX
PA   (INTE-) INTERLEUKIN GENETICS INC.
XX
PI   Duff G,  Kornman K,  Van Dijk S;
XX
DR   WPI; 2004-354679/33.
XX
PT   Determining the predisposition to early-onset menopause comprises
PT   detecting in the subject interleukin (IL)-1RN (+2018) allele 2.
XX
PS   Example; SEQ ID NO 9; 57pp; English.
XX
CC   The present invention provides a method for determining the
CC   predisposition of a subject to early-onset menopause (EOM). The invention
CC   is useful in diagnosing, treating and preventing early-onset menopause.
CC   The present sequence is human secreted interleukin-1RN (IL-1RN)
CC   amplifying PCR primer. The sequence is used in exemplification of the
CC   invention.
XX
SQ   Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 21
ADO35276
ID   ADO35276 standard; DNA; 17 BP.
XX
AC   ADO35276;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Human interleukin-1RN (IL-1RN) gene, PCR primer #1.
XX
KW   human; obstructive airway disease; OAD; interleukin-13; IL-13; IL-1B;
KW   IL-1A; IL-1RN; asthma; interleukin-1A; interleukin-1B; interleukin-1RN;
KW   ss; primer.
XX
OS   Homo sapiens.
XX
PN   US6746839-B1.
XX
PD   08-JUN-2004.
XX
PF   01-JUN-2000; 2000US-00584950.
XX
PR   12-JAN-1998;   98US-00005923.
XX
PA   (INTE-) INTERLEUKIN GENETICS INC.
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XX
PI   Duff GW,  Di Giovine FS,  Barnes PJ,  Lim S;
XX
DR   WPI; 2004-429802/40.
XX
PT   Determining whether a subject has or is predisposed to developing an
PT   obstructive airway disease (OAD), such as asthma, detecting an OAD-
PT   associated allele in a nucleic acid sample from the subject, which
PT   indicates predisposition to OAD.
XX
PS   Example 3; SEQ ID NO 13; 61pp; English.
XX
CC   The invention relates to a method of determining whether a subject has,
CC   or is predisposed to developing, an obstructive airway disease (OAD),
CC   comprising detecting an OAD-associated allele in a nucleic acid sample
CC   from the subject, where the presence of OAD-associated allele indicates
CC   that the subject has or is predisposed to the development of OAD. The OAD
CC   associated allele is selected from allele 2 of interleukin-13 (IL-13)
CC   (+2581), allele 2 of IL-1B (-511), allele 2 of IL-1B (+3954), or an
CC   allele in linkage disequilibrium with allele 2 of IL-1B (-511) or allele
CC   2 of IL-1B (+3954) comprising allele 4 of IL-1A (222/223), allele 4 of IL
CC   -1A (gz5/gz6), allele 1 of IL-1A (-889), allele 1 of (+3954), allele 3 of
CC   the gaat.p33330 marker, allele 3 of the Y31 marker, allele 2 of IL-1RN
CC   (+2018), allele 2 of IL-1RN (VNTR), allele 3 of IL-1A (222/223), allele 3
CC   of IL-1A (gz5/gz6), allele 2 of IL-1A(-889), allele 1 of IL-1B (-511),
CC   allele 4 of the gaat.p33330 marker, allele 6 of the Y31 marker, allele 1
CC   of IL-1RN (+2018), and allele 1 of IL-1RN (VNTR). The method is useful
CC   for determining whether a subject has or is predisposed to developing an
CC   OAD, particularly asthma. The method is especially useful for the early
CC   identification of those who are generally susceptible to OAD, and those
CC   who are susceptible to acute episodes. Early identification would
CC   facilitate the prevention or administration of appropriate treatment at
CC   the earliest stage, thus increasing the probability of a positive
CC   outcome. The present sequence represents a PCR primer used to detect
CC   polymorphisms in the human interleukin-1 (IL-1) gene locus.
XX
SQ   Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 22
ADU16279
ID   ADU16279 standard; DNA; 17 BP.
XX
AC   ADU16279;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Human interleukin-1R genotyping primer seqid 29.
XX
KW   seronegative spondyloarthropathy; interleukin 1; IL-1;
KW   ankylosing spondylitis; interleukin-1R; IL-1R; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO2004097045-A1.
XX
PD   11-NOV-2004.
XX
PF   04-MAY-2004; 2004WO-GB001905.
XX
PR   01-MAY-2003; 2003GB-00010060.
XX
PA   (ISIS-) ISIS INNOVATION LTD.
XX
PI   Brown MA;
XX
DR   WPI; 2004-804774/79.
XX
PT   Detecting, in vitro, whether a subject has or is genetically predisposed
PT   to a seronegative spondyloarthropathy comprises determining the presence
PT   of a polymorphism in interleukin 1 gene region of chromosome 2.
XX
PS   Example; SEQ ID NO 29; 40pp; English.
XX
CC   The invention describes a method of detecting, in vitro, whether a
CC   subject has or is genetically predisposed to a seronegative
CC   spondyloarthropathy comprises determining the presence of a genetic
CC   polymorphism within the interleukin 1 (IL-1) gene region of chromosome 2
CC   extending from IL-1A to the beginning of IL-1RN in a genetic sample
CC   obtained from a subject. Also described are: an isolated polynucleotide,
CC   useful for diagnosing whether a subject has or is predisposed to a
CC   seronegative spondyloarthropathy, comprising at least a contiguous
CC   sequence of 15 bases derived from the IL-1 gene region, or its complement
CC   ; and a diagnostic kit comprising the polynucleotide. The polynucleotide
CC   is useful for determining whether a subject has or is predisposed to a
CC   seronegative spondyloarthropathy. The method and kit are useful for
CC   diagnosing seronegative spondyloarthropathy, i.e. ankylosing spondylitis.
CC   This sequence represents an interleukin-1R (IL-1R) primer used to
CC   genotype the IL-1R gene.
XX
SQ   Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 23
ADU48041
ID   ADU48041 standard; DNA; 17 BP.
XX
AC   ADU48041;
XX
DT   10-FEB-2005  (first entry)
XX
DE   Human IL-1A (VNTR) polymorphic locus amplifying PCR primer #1.
XX
KW   Restenosis; interleukin; IL; IL-1A; IL-1B; IL-1RN; vasotropic; human;
KW   PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2004229264-A1.
XX
PD   18-NOV-2004.
XX
PF   12-APR-2004; 2004US-00823197.
XX
PR   10-MAR-1997;   97US-00813456.
PR   26-MAY-1999;   99US-00320395.
PR   01-NOV-1999;   99US-00431352.
PR   24-MAY-2000; 2000US-00578534.
XX
PA   (INTE-) INTERLEUKIN GENETICS INC.
XX
PI   Crossman DC,  Duff GW,  Francis SE,  Kornman KS,  Stephenson K;
XX
DR   WPI; 2004-813241/80.
XX
PT   New kit comprises a first primer oligonucleotide that hybridizes 5' or 3'
PT   to an allele 1 of IL-1A (+4845), IL-1B (-511), IL-1B (+3954), IL-1RN
PT   (VNTR), or IL-1RN (+2018), useful for diagnosing, treating, or preventing
PT   restenosis.
XX
```

```
PS   Claim 11; SEQ ID NO 7; 81pp; English.
XX
CC   The invention relates to a kit for determining the existence of or a
CC   susceptibility to developing a restenosis in a subject. The kit comprises
CC   of a primer that hybridises 5' or 3' to an allele selected from allele 1
CC   of the following markers, interleukin (IL)-1A (+4845), IL-1B (-511), IL-
CC   1B (+3954), IL-1RN (VNTR) or IL-1RN (+2018) or an allele in linkage
CC   disequilibrium with it. The kit is useful for determining the existence
CC   of or a susceptibility to developing a restenosis in a subject. It is
CC   also useful for determining whether a subject has or is predisposed to
CC   developing restenosis or for treating or preventing restenosis. The
CC   present sequence is a PCR primer used for amplifying human IL-1A gene
CC   polymorphic locus.
XX
SQ   Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 24
ADY72754
ID   ADY72754 standard; DNA; 17 BP.
XX
AC   ADY72754;
XX
DT   02-JUN-2005  (first entry)
XX
DE   Human IL-1RN PCR primer SEQ ID NO:5.
XX
KW   interleukin-1 receptor; menopause; gynecological; gynecology; obstetrics;
KW   metabolic disorder; PCR; primer; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US2005064453-A1.
XX
PD   24-MAR-2005.
XX
PF   03-MAY-2004; 2004US-00838503.
XX
PR   30-JUN-1999;   99US-00345217.
PR   04-AUG-2000; 2000US-00632657.
XX
PA   (DUFF/) DUFF G.
PA   (KORN/) KORNMAN K.
PA   (DIJK/) DIJK S V.
XX
PI   Duff G,  Kornman K,  Dijk SV;
XX
DR   WPI; 2005-241272/25.
XX
PT   New kit for determining a woman's predisposition to early-onset menopause
PT   (EOM) comprises primers that hybridize to a marker of an IL-1-related
PT   gene associated with EOM, a DNA sampling means, a control, and a DNA
PT   detection means.
XX
PS   Claim 5; SEQ ID NO 5; 59pp; English.
XX
CC   The invention relates to a kit for determining a woman's predisposition
CC   to early-onset menopause (EOM). The kit comprises a first primer that
CC   hybridizes 5' or 3' to a marker of an IL-1-related gene associated with
CC   early-onset menopause. Gynecological. The kit is useful for detecting a
CC   predisposition to EOM, for treating or preventing the development of EOM
CC   in a woman, or for identifying agents that may treat or prevent EOM. The
CC   present sequence represents a PCR primer for the human interleukin 1
CC   receptor antagonist (IL-1RN) gene, which is used in an example from the
CC   present invention for determining an individuals allelic pattern
CC   (genotyping). The human IL-1RN gene is located on chromosome 2, more
CC   specifically to q13-14.1. Note: the present sequence is designated SEQ ID
CC   NO:5 in the examples and claims, but corresponds with SEQ ID NO:9 in the
CC   Sequence Listing.
XX
SQ   Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 25
AEE01079
ID   AEE01079 standard; DNA; 17 BP.
XX
AC   AEE01079;
XX
DT   26-JAN-2006  (first entry)
XX
DE   Human interleukin (IL)-1 PCR primer SEQ ID NO 22.
XX
KW   periodontal disease; interleukin; IL-1; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO2005108619-A2.
XX
PD   17-NOV-2005.
XX
PF   03-MAY-2005; 2005WO-US015267.
XX
PR   03-MAY-2004; 2004US-0567727P.
XX
PA   (INTE-) INTERLEUKIN GENETICS INC.
XX
PI   Duff GW,  Kornman K,  Wilkins L,  Chen HM,  Rogus J;
XX
DR   WPI; 2005-811015/82.
XX
PT   Identifying a subject having increased IL-1B transcription, for
PT   identifying if the subject is predisposed to periodontal disease, by
PT   providing a biological sample comprising genomic DNA, and identifying an
PT   IL-1B allele in the sample.
XX
PS   Example 1; SEQ ID NO 22; 126pp; English.
XX
CC   The invention relates to a method of identifying a subject having
CC   increased IL-1B transcription providing a biological sample comprising
CC   genomic DNA from the subject, and identifying an IL-1B allele selected
CC   from IL-1B (-3737) allele 1 and/or IL-1B (-1468) allele 1 in the sample,
CC   where the presence of the allele indicates that the subject has increased
CC   IL-1B transcription. The methods are useful for identifying if the
CC   subject is predisposed to periodontal disease, and as assays for
CC   identifying therapeutics for treating and/or preventing the development
CC   of the disease. The present sequence represents a human interleukin (IL)-
CC   1 PCR primer.
XX
SQ   Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17
```

RESULT 26
ACC44794
ID ACC44794 standard; DNA; 17 BP.
XX
AC ACC44794;
XX
DT 03-JUN-2003 (first entry)
XX
DE Interleukin 1 beta PCR primer SEQ ID NO:5.
XX
KW Interleukin 1 beta; IL-1 beta; hepatitis C virus; HCV; infection;
KW liver cancer; cytostatic; PCR primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003016570-A1.
XX
PD 27-FEB-2003.
XX
PF 21-AUG-2002; 2002WO-JP008415.
XX
PR 21-AUG-2001; 2001JP-00250545.
XX
PA (HUBI-) HUBIT GENOMIX INC.
XX
PI Omata M, Kato N;
XX
DR WPI; 2003-256715/25.
XX
PT Examining liver cell cancer particularly after infection with hepatitis
PT virus by using polymorphism of IL-1beta gene, also applicable in
PT screening preventives or remedies for liver cell cancer.
XX
PS Example 2; Page 33; 55pp; Japanese.
XX
CC The present invention describes a method for examining liver cell cancer
CC caused by hepatitis virus, where the method comprises the detection of a
CC polymorphism produced at the promoter region of interleukin 1 (IL-1) beta
CC gene. IL-1 beta has cytostatic activity. The method is for examining
CC liver cell cancer particularly after infection with hepatitis C virus
CC (HCV), which can also be applied in screening drugs for the prevention or
CC treatment of liver cell cancer. The present sequence represents a PCR
CC primer for IL-1 beta, which is used in an example from the present
CC invention
XX
SQ Sequence 17 BP; 4 A; 10 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 82.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCC 14
||||||||||||||
Db 4 CTCAGCAACACTCC 17

RESULT 27
ADU50588
ID ADU50588 standard; DNA; 17 BP.
XX
AC ADU50588;
XX
DT 10-FEB-2005 (first entry)
XX
DE IL-1RN VNTR polymorphism PCR primer, SEQ ID 9.
XX
KW Immunosuppressive; Gene Therapy; kidney; interleukin-1; PCR; primer; ss.
XX
OS Synthetic.
XX
PN US2004229228-A1.
XX
PD 18-NOV-2004.
XX
PF 24-JUL-2003; 2003US-00626830.
XX
PR 25-JUL-2002; 2002US-0398986P.
XX
PA (NOUN) UNIV NORTHWESTERN.
PA (AMGE-) AMGEN INC.
XX
PI Sims JE, Kaufman DB;
XX
DR WPI; 2005-010687/01.
XX
PT Diagnosing early kidney allograft rejection comprises determining a
PT genotype of an IL-1 family member gene.
XX
PS Example 1; SEQ ID NO 9; 12pp; English.
XX
CC The present invention relates to a method for identifying an individual
CC predisposed to early rejection of a kidney allograft. The method
CC comprises determining a genotype of an interleukin-1 (IL-1) family member
CC gene, where the presence of one or more alleles, e.g. an A1,A2 allele
CC combination at an IL-1A VNTR intron 6 locus, an A2 allele at an IL-
CC 1A+4845 locus, or an E2 allele at an IL-1B+3953 locus indicates that the
CC individual is at increased risk for early rejection of the kidney
CC allograft. Also claimed is a primer set for determining a genotype in an
CC IL-1 family member gene. The present sequence is one such primer. The
CC methods and primers are useful for identifying an individual predisposed
CC to and treating a patient predisposed to early rejection of a kidney
CC allograft.
XX
SQ Sequence 17 BP; 4 A; 10 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 82.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCC 14
||||||||||||||
Db 4 CTCAGCAACACTCC 17

RESULT 28
AAD48159/c
ID AAD48159 standard; DNA; 16 BP.
XX
AC AAD48159;
XX
DT 24-FEB-2003 (first entry)
XX
DE PCR primer #7 used for single nucleotide polymorphism (SNP) analysis.
XX
KW Peptide nucleic acid; PNA; nucleic acid zygosity; genetic analysis;
KW scientific investigation; pharmacogenomic; pharmacogenetic; epigenomic;
KW PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO200272865-A2.
XX
PD 19-SEP-2002.
XX
PF 09-MAR-2002; 2002WO-US007050.
XX
PR 09-MAR-2001; 2001US-0274547P.
XX
PA (BOST-) BOSTON PROBES INC.
XX
PI Coull JM, Fiandaca MJ, Kristjanson MD, Hyldig-Nielsen JJ;
PI Creasey TM;
XX
DR WPI; 2003-018741/01.

```
XX
PT   Composition for determining target sequence of contiguous nucleobases,
PT   comprises polynucleobase strand and combination oligomer comprising first
PT   and second oligomer blocks that are covalently linked to each other.
XX
PS   Example 5; Page 70; 149pp; English.
XX
CC   The present invention relates to combination oligomers, including block
CC   synthesis of combination of oligomers in the absence of a template. The
CC   invention relates to a composition comprising a polynucleobase strand and
CC   a combination oligomer comprising first and second oligomer blocks that
CC   are each independently a peptide nucleic acid (PNA) covalently linked to
CC   each other by a linker of at least three atoms in length, where the
CC   oligomer blocks are sequences specifically hybridised to a target
CC   sequence of contiguous nucleobases in the polynucleobase strand, to form
CC   a double stranded target sequence-oligomer complex. The composition is
CC   used for determining a target sequence of contiguous nucleobases and for
CC   determining the zygosity of a nucleic acid for a single nucleotide
CC   polymorphism (SNP). The methods are useful in scientific investigation,
CC   e.g., for detection, identification and/or enumeration of bacteria,
CC   viruses and pathogens in food, beverages, water, pharmaceutical products,
CC   personal care products, dairy products, in clinical samples or in samples
CC   of plant, animal, human or environmental origin. They are also useful for
CC   the analysis of raw materials, equipment, products or processes used to
CC   manufacture or store food, beverages, water, pharmaceutical products,
CC   personal care products dairy products or environmental samples. The
CC   methods and materials are useful in areas such as expression analysis,
CC   SNP analysis, genetic analysis of humans, animals, fungi, yeast viruses
CC   and plants, therapy monitoring, pharmacogenomics, pharmacogenetics,
CC   epigenomics and high throughput screening operations. The present
CC   sequence is a PCR primer used for single nucleotide polymorphism (SNP)
CC   analysis
XX
SQ   Sequence 16 BP; 3 A; 1 C; 8 G; 4 T; 0 U; 0 Other;

  Query Match             72.9%;  Score 12.4;  DB 1;  Length 16;
  Best Local Similarity   92.9%;  Pred. No. 68;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TCAGCAACACTCCT 15
              |||||| |||||||
Db         15 TCAGCACCACTCCT 2


RESULT 29
ACN01682
ID   ACN01682 standard; RNA; 17 BP.
XX
AC   ACN01682;
XX
DT   22-APR-2004  (first entry)
XX
DE   WNV Inozyme substrate SEQ ID NO 1672.
XX
KW   WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW   virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW   encephalitis; myocarditis; meningitis; infection; hepatitis;
KW   liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KW   Amberzyme; Zinzyme; ss.
XX
OS   West Nile Virus.
XX
PN   WO200268637-A2.
XX
PD   06-SEP-2002.
XX
PF   19-OCT-2001; 2001WO-US048350.
XX
PR   20-OCT-2000; 2000US-0242411P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MCSW/) MCSWIGGEN J A.
XX
PI   Blatt L,  Mcswiggen JA;
XX
DR   WPI; 2002-706994/76.
XX
PT   New nucleic acid molecule that modulates replication of West Nile Virus
PT   (WNV), useful for treating a condition related to WNV infection e.g.
PT   pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS   Claim 23; SEQ ID NO 1672; 495pp; English.
XX
CC   The invention relates to nucleic acid molecules that modulate replication
CC   of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC   treating a condition related to WNV infection e.g. pancreatitis,
CC   encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC   liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC   molecule is selected from the group of ribozymes consisting of
CC   Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
CC   nucleic acid molecules further comprise at least five ribose residues, at
CC   least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC   least three of the 5' terminal nucleotides and a 3' end modification of a
CC   3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC   are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC   in the specification. The present sequence is that of a nucleic acid
CC   molecule of the invention
XX
SQ   Sequence 17 BP; 4 A; 6 C; 2 G; 0 T; 5 U; 0 Other;

  Query Match             72.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   71.4%;  Pred. No. 74;
  Matches   10;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TCAGCAACACTCCT 15
              :||||| |||:||:
Db          4 UCAGCAUCACUCCU 17


RESULT 30
ACN01683
ID   ACN01683 standard; RNA; 17 BP.
XX
AC   ACN01683;
XX
DT   22-APR-2004  (first entry)
XX
DE   WNV Inozyme substrate SEQ ID NO 1673.
XX
KW   WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW   virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW   encephalitis; myocarditis; meningitis; infection; hepatitis;
KW   liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KW   Amberzyme; Zinzyme; ss.
XX
OS   West Nile Virus.
XX
PN   WO200268637-A2.
XX
PD   06-SEP-2002.
XX
PF   19-OCT-2001; 2001WO-US048350.
XX
PR   20-OCT-2000; 2000US-0242411P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MCSW/) MCSWIGGEN J A.
XX
PI   Blatt L,  Mcswiggen JA;
XX
DR   WPI; 2002-706994/76.
XX
PT   New nucleic acid molecule that modulates replication of West Nile Virus
PT   (WNV), useful for treating a condition related to WNV infection e.g.
```

PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 23; SEQ ID NO 1673; 495pp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 3 A; 7 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 72.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 74;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TCAGCAACACTCCT 15
:||||| |||:||:
Db 1 UCAGCAUCACUCCU 14

RESULT 31
ACN00198
ID ACN00198 standard; RNA; 17 BP.
XX
AC ACN00198;
XX
DT 22-APR-2004 (first entry)
XX
DE WNV Hammerhead Ribozyme substrate SEQ ID NO 188.
XX
KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KW Amberzyme; Zinzyme; ss.
XX
OS West Nile Virus.
XX
PN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
PI Blatt L, Mcswiggen JA;
XX
DR WPI; 2002-706994/76.
XX
PT New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 23; SEQ ID NO 188; 495pp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 3 A; 7 C; 2 G; 0 T; 5 U; 0 Other;

Query Match 72.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 74;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TCAGCAACACTCCT 15
:||||| |||:||:
Db 2 UCAGCAUCACUCCU 15

RESULT 32
ACN14095/c
ID ACN14095 standard; RNA; 17 BP.
XX
AC ACN14095;
XX
DT 22-APR-2004 (first entry)
XX
DE WNV minus strand DNAzyme substrate SEQ ID NO 14098.
XX
KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KW Amberzyme; Zinzyme; ss.
XX
OS West Nile Virus.
XX
PN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
PI Blatt L, Mcswiggen JA;
XX
DR WPI; 2002-706994/76.
XX
PT New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 23; SEQ ID NO 14098; 495pp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a

```
CC   3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC   are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC   in the specification. The present sequence is that of a nucleic acid
CC   molecule of the invention
XX
SQ   Sequence 17 BP; 5 A; 2 C; 6 G; 0 T; 4 U; 0 Other;

  Query Match             72.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 74;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TCAGCAACACTCCT 15
              |||||| |||||||
Db         15 TCAGCATCACTCCT 2


RESULT 33
ACN15151/c
ID   ACN15151 standard; RNA; 17 BP.
XX
AC   ACN15151;
XX
DT   22-APR-2004  (first entry)
XX
DE   WNV minus strand Amberzyme substrate SEQ ID NO 15154.
XX
KW   WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW   virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW   encephalitis; myocarditis; meningitis; infection; hepatitis;
KW   liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KW   Amberzyme; Zinzyme; ss.
XX
OS   West Nile Virus.
XX
PN   WO200268637-A2.
XX
PD   06-SEP-2002.
XX
PF   19-OCT-2001; 2001WO-US048350.
XX
PR   20-OCT-2000; 2000US-0242411P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MCSW/) MCSWIGGEN J A.
XX
PI   Blatt L,  Mcswiggen JA;
XX
DR   WPI; 2002-706994/76.
XX
PT   New nucleic acid molecule that modulates replication of West Nile Virus
PT   (WNV), useful for treating a condition related to WNV infection e.g.
PT   pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS   Claim 23; SEQ ID NO 15154; 495pp; English.
XX
CC   The invention relates to nucleic acid molecules that modulate replication
CC   of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC   treating a condition related to WNV infection e.g. pancreatitis,
CC   encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC   liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC   molecule is selected from the group of ribozymes consisting of
CC   Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
CC   nucleic acid molecules further comprise at least five ribose residues, at
CC   least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC   least three of the 5' terminal nucleotides and a 3' end modification of a
CC   3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC   are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC   in the specification. The present sequence is that of a nucleic acid
CC   molecule of the invention
XX
SQ   Sequence 17 BP; 5 A; 2 C; 7 G; 0 T; 3 U; 0 Other;

  Query Match             72.9%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 74;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TCAGCAACACTCCT 15
              |||||| |||||||
Db         16 TCAGCATCACTCCT 3


RESULT 34
ABI02395/c
ID   ABI02395 standard; DNA; 12 BP.
XX
AC   ABI02395;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 302368 for detecting SNP TSC0019966.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 302368; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             64.7%;  Score 11;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 76;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCTA 16
              |||||||||||
Db         11 CAACACTCCTA 1


RESULT 35
ABK72568
ID   ABK72568 standard; DNA; 12 BP.
XX
```

AC ABK72568;
XX
DT 13-AUG-2002 (first entry)
XX
DE Human OPA1 gene, exon/intron junction #35.
XX
KW Human; ophthalmological; OPA1; autosomal dominant optic atrophy; ADOA;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200227022-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-GB004284.
XX
PR 26-SEP-2000; 2000GB-00023555.
XX
PA (UNLO) UNIV COLLEGE LONDON.
PA (UYEY-) UNIV EYE HOSPITAL.
XX
PI Bhattacharya S, Wissinger B, Alexander C, Votruba M;
XX
DR WPI; 2002-416484/44.
XX
PT Novel human normal or mutant OPA1 (the predominant locus for autosomal
PT dominant optic atrophy (ADOA)) polypeptides and the OPA1 gene, useful in
PT the diagnosis and treatment of autosomal dominant optic atrophy ADOA.
XX
PS Disclosure; Fig 12; 75pp; English.
XX
CC The invention relates to an isolated human normal or mutant OPA1 (the
CC predominant locus for autosomal dominant optic atrophy (ADOA))
CC polypeptide (I), characterised by a molecular weight of about 112 kDa,
CC and substantially free of other human proteins. Also described is the DNA
CC (II) encoding (I). (I) and (II) are useful as a medicament, for the
CC treatment of a medical condition resulting from a defect in the OPA1
CC gene, which results in autosomal dominant optic atrophy. The nucleic acid
CC and antibodies to (I) are useful in a variety of hybridisation and
CC immunological assays to screen for, and to detect the presence of, either
CC a normal or a defective OPA1 gene or gene product. ABK72533-ABK72593
CC represent the human OPA1 gene and intron/exon splice junctions
XX
SQ Sequence 12 BP; 4 A; 6 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 64.7%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACAC 11
||||||||||
Db 2 CTCAGCAACAC 12

RESULT 36
ABF36021
ID ABF36021 standard; DNA; 13 BP.
XX
AC ABF36021;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 136018 for detecting SNP TSC0033969.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 136018; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 6 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 64.7%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AACACTCCTAT 17
||||||||||
Db 2 AACACTCCTAT 12

RESULT 37
ABC71077
ID ABC71077 standard; DNA; 13 BP.
XX
AC ABC71077;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 71094 for detecting SNP TSC0018437.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is

```
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 71094; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             64.7%;  Score 11;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 84;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCTA 16
              ||||||||||
Db          1 CAACACTCCTA 11


RESULT 38
ABF36020/c
ID   ABF36020 standard; DNA; 13 BP.
XX
AC   ABF36020;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 136017 for detecting SNP TSC0033969.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 136017; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             64.7%;  Score 11;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 84;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 AACACTCCTAT 17
              ||||||||||
Db         12 AACACTCCTAT 2


RESULT 39
ABC71076/c
ID   ABC71076 standard; DNA; 13 BP.
XX
AC   ABC71076;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 71093 for detecting SNP TSC0018437.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 71093; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             64.7%;  Score 11;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 84;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCTA 16
              ||||||||||
```

```
Db         13 CAACACTCCTA 3


RESULT 40
ABX03942/c
ID   ABX03942 standard; DNA; 15 BP.
XX
AC   ABX03942;
XX
DT   09-JAN-2003  (first entry)
XX
DE   S. cerevisiae 28S rRNA fragment.
XX
KW   Detection; probe; diagnosis; oral disease; paradontitis; caries; therapy;
KW   polymorphism; virulence factor; antibiotic resistance gene; prognosis;
KW   oral infection; detection; pathogen; coronary heart disease;
KW   diabetic symptom; ss.
XX
OS   Saccharomyces cerevisiae.
XX
PN   DE20110013-U1.
XX
PD   18-OCT-2001.
XX
PF   13-MAR-2001; 2001DE-02010013.
XX
PR   13-MAR-2001; 2001DE-01012348.
PR   13-MAR-2001; 2001DE-02010013.
XX
PA   (ROET/) ROETGER A.
XX
DR   WPI; 2001-657777/76.
XX
PT   Oligonucleotide array, useful for diagnosing oral diseases, particularly
PT   paradontitis, carries human or microbial reference sequences.
XX
PS   Claim 8; Page 22; 58pp; German.
XX
CC   This invention describes a novel nucleotide carrier with probes used for
CC   diagnosis of oral diseases, particularly paradontitis, but also caries,
CC   especially to identify genetic predisposition (as indicated by
CC   polymorphisms) to disease and to identify causative microorganisms or
CC   their associated virulence factors and antibiotic resistance genes, e.g.
CC   for selection of therapy and for prognosis. They are also useful for
CC   research into oral infections. The carriers allow simultaneous detection
CC   of both host and pathogen parameters, providing quickly and simply an
CC   individual's paradontitis profile, including detection of pathogens that
CC   are associated with increased risk of coronary heart diseases and/or
CC   aggravation of diabetic symptoms, and of opportunistic pathogens.
CC   ABX03870-ABX04044 represent DNA fragments used to illustrate the method
CC   of the invention
XX
SQ   Sequence 15 BP; 5 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             63.5%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 1.1e+02;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 AGCAACACTCCTAT 17
              ||| ||| ||||||
Db         15 AGCTACATTCCTAT 2


RESULT 41
ABH90683/c
ID   ABH90683 standard; DNA; 12 BP.
XX
AC   ABH90683;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 290676 for detecting SNP TSC0014465.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 290676; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             61.2%;  Score 10.4;  DB 1;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 93;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCTAT 17
              ||| ||||||||
Db         12 CAAAACTCCTAT 1


RESULT 42
ABI59938/c
ID   ABI59938 standard; DNA; 12 BP.
XX
AC   ABI59938;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 359911 for detecting SNP TSC0051838.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
```

```
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 359911; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             61.2%;  Score 10.4;  DB 1;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 93;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCTAT 17
              ||||| ||||||
Db         12 CAACATTCCTAT 1


RESULT 43
ABC51750/c
ID   ABC51750 standard; DNA; 13 BP.
XX
AC   ABC51750;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 51767 for detecting SNP TSC0014432.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 51767; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             61.2%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 1e+02;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCTAT 17
              ||||| ||||||
Db         13 CAACATTCCTAT 2


RESULT 44
ABF59814/c
ID   ABF59814 standard; DNA; 13 BP.
XX
AC   ABF59814;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 159811 for detecting SNP TSC0040225.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 159811; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
```

```
SQ   Sequence 13 BP; 1 A; 0 C; 6 G; 5 T; 0 U; 1 Other;

  Query Match            61.2%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity  91.7%;  Pred. No. 1e+02;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CAGCAACACTCC 14
              || |||||||||
Db         12 CAACAACACTCC 1


RESULT 45
ABF91047
ID   ABF91047 standard; DNA; 13 BP.
XX
AC   ABF91047;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 191044 for detecting SNP TSC0047001.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 191044; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match            61.2%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity  91.7%;  Pred. No. 1e+02;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCTAT 17
              || |||||||||
Db          2 CACCACTCCTAT 13


RESULT 46
ABH23826/c
ID   ABH23826 standard; DNA; 13 BP.
XX
AC   ABH23826;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 223803 for detecting SNP TSC0054492.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 223803; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match            61.2%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity  91.7%;  Pred. No. 1e+02;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCTAT 17
              ||||| ||||||
Db         13 CAACATTCCTAT 2


RESULT 47
ABF63332/c
ID   ABF63332 standard; DNA; 13 BP.
XX
AC   ABF63332;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 163329 for detecting SNP TSC0041059.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
```

```
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 163329; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 0 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             61.2%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 1e+02;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 AGCAACACTCCT 15
              | ||||||||||
Db         12 ACCAACACTCCT 1


RESULT 48
ABF79990/c
ID   ABF79990 standard; DNA; 13 BP.
XX
AC   ABF79990;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 179987 for detecting SNP TSC0044568.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 179987; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             61.2%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 1e+02;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACT 12
              |||| |||||||
Db         12 CTCATCAACACT 1


RESULT 49
ABF63333
ID   ABF63333 standard; DNA; 13 BP.
XX
AC   ABF63333;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 163330 for detecting SNP TSC0041059.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 163330; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
```

```
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match            61.2%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity  91.7%;  Pred. No. 1e+02;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 AGCAACACTCCT 15
              | ||||||||||
Db          2 ACCAACACTCCT 13


RESULT 50
ABH62283
ID   ABH62283 standard; DNA; 13 BP.
XX
AC   ABH62283;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 262260 for detecting SNP TSC0010773.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 262260; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match            61.2%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity  91.7%;  Pred. No. 1e+02;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCTAT 17
              |||| |||||||
Db          1 CAACCCTCCTAT 12


Search completed: November 21, 2006, 14:29:06
Job time : 0.001 secs
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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: November 21, 2006, 14:33:58 ; Search time 0.001 Seconds
(without alignments)
6.358 Million cell updates/sec

Title: US-10-823-197-7
Perfect score: 17
Sequence: 1 CTCAGCAACACTCCTAT 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 16 seqs, 187 residues

Total number of hits satisfying chosen parameters: 32

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 16 summaries

Database : rnpbndb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	100.0	17	1	US-11-203-682-90	Sequence 90, Appl
2	17	100.0	17	1	US-11-283-168-1	Sequence 1, Appli
3	8.4	49.4	11	1	US-11-364-118-4	Sequence 4, Appli
4	8.4	49.4	11	1	US-11-364-118-229	Sequence 229, App
c 5	8.4	49.4	11	1	US-11-158-209-97	Sequence 97, Appl
c 6	8.4	49.4	11	1	US-11-158-209-545	Sequence 545, App
7	8.4	49.4	12	1	US-11-212-812A-395	Sequence 395, App
8	8.4	49.4	12	1	US-11-212-386A-395	Sequence 395, App
c 9	8	47.1	11	1	US-11-364-118-390	Sequence 390, App
c 10	8	47.1	11	1	US-11-364-118-457	Sequence 457, App
c 11	7.8	45.9	11	1	US-11-158-209-691	Sequence 691, App
c 12	7.8	45.9	11	1	US-11-158-209-1221	Sequence 1221, Ap
13	7.8	45.9	11	1	US-11-148-303-66	Sequence 66, Appl
c 14	7.4	43.5	10	1	US-10-691-012-35	Sequence 35, Appl
15	7.4	43.5	10	1	US-11-148-303-23	Sequence 23, Appl
16	7.4	43.5	10	1	US-11-148-303-128	Sequence 128, App

ALIGNMENTS

RESULT 1
US-11-203-682-90
; Sequence 90, Application US/11203682
; Publication No. US20060183161A1
; GENERAL INFORMATION:
; APPLICANT: Nicklin, Martin
; APPLICANT: Barton, Jenny
; TITLE OF INVENTION: IL-1L1 GENE AND POLYPEPTIDE PRODUCTS
; FILE REFERENCE: 24299-517 CIP
; CURRENT APPLICATION NUMBER: US/11/203,682
; CURRENT FILING DATE: 2005-08-12
; PRIOR APPLICATION NUMBER: 09/617,720
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 90
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized primer
US-11-203-682-90

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
||||||||||||||||||
Db 1 CTCAGCAACACTCCTAT 17

RESULT 2
US-11-283-168-1
; Sequence 1, Application US/11283168
; Publication No. US20060252055A1
; GENERAL INFORMATION:
; APPLICANT: Francis, Sheila E
; APPLICANT: Crossman, David C
; APPLICANT: Duff, Gordon W
; APPLICANT: Kornman, Kenneth S
; APPLICANT: Martinez, Katherine
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR CARDIOVASCULAR DISORDERS
; FILE REFERENCE: 24299-504 CIP2 CON CIP1
; CURRENT APPLICATION NUMBER: US/11/283,168
; CURRENT FILING DATE: 2005-11-17
; PRIOR APPLICATION NUMBER: 10/320,360
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 09/431,352
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 09/320,395
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 08/813,456
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Primer
US-11-283-168-1

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
||||||||||||||||||
Db 1 CTCAGCAACACTCCTAT 17

RESULT 3
US-11-364-118-4
; Sequence 4, Application US/11364118
; Publication No. US20060204992A1
; GENERAL INFORMATION:
; APPLICANT: Olaf Holtkotter
; APPLICANT: Dirk Petersohn
; APPLICANT: Kordula Schlotmann
; APPLICANT: Melanie Giesen
; APPLICANT: Daniela Kessler-Becker
; TITLE OF INVENTION: Method for Determining Hair Cycle Markers
; FILE REFERENCE: H 06059 PCT

```
;  CURRENT APPLICATION NUMBER: US/11/364,118
;  CURRENT FILING DATE:  2006-02-28
;  PRIOR APPLICATION NUMBER: PCT/EP2004/009435
;  PRIOR FILING DATE: 2004-08-24
;  PRIOR APPLICATION NUMBER: 103 40 373.6-41
;  PRIOR FILING DATE: 2003-08-30
;  NUMBER OF SEQ ID NOS: 570
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 4
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-364-118-4

  Query Match             49.4%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 6.6;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCT 15
              ||||| ||||
Db          1 CAACATTCCT 10


RESULT 4
US-11-364-118-229
; Sequence 229, Application US/11364118
; Publication No. US20060204992A1
; GENERAL INFORMATION:
;  APPLICANT: Olaf Holtkotter
;  APPLICANT:  Dirk Petersohn
;  APPLICANT:  Kordula Schlotmann
;  APPLICANT:  Melanie Giesen
;  APPLICANT:  Daniela Kessler-Becker
;  TITLE OF INVENTION: Method for Determining Hair Cycle Markers
;  FILE REFERENCE: H 06059 PCT
;  CURRENT APPLICATION NUMBER: US/11/364,118
;  CURRENT FILING DATE:  2006-02-28
;  PRIOR APPLICATION NUMBER: PCT/EP2004/009435
;  PRIOR FILING DATE: 2004-08-24
;  PRIOR APPLICATION NUMBER: 103 40 373.6-41
;  PRIOR FILING DATE: 2003-08-30
;  NUMBER OF SEQ ID NOS: 570
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 229
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-364-118-229

  Query Match             49.4%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 6.6;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCT 15
              ||||| ||||
Db          1 CAACATTCCT 10


RESULT 5
US-11-158-209-97/c
; Sequence 97, Application US/11158209
; Publication No. US20060088852A1
; GENERAL INFORMATION:
;  APPLICANT: Dirk Petersohn
;  APPLICANT:  Kordula Schlotmann
;  APPLICANT:  Thomas Gassenmeier
;  APPLICANT:  Olaf Holtkotter
;  APPLICANT:  Marcus Conradt
;  APPLICANT:  Kay Hofmann
;  TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
;  FILE REFERENCE: H 05667 PCT
;  CURRENT APPLICATION NUMBER: US/11/158,209
;  CURRENT FILING DATE:  2005-06-20
;  PRIOR APPLICATION NUMBER: PCT/EP2003/014070
;  PRIOR FILING DATE: 2003-12-11
;  PRIOR APPLICATION NUMBER: 102 60 931.4-41
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 1335
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 97
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-158-209-97

  Query Match             49.4%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 6.6;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACA 10
              | ||||||||
Db         11 CCCAGCAACA 2


RESULT 6
US-11-158-209-545/c
; Sequence 545, Application US/11158209
; Publication No. US20060088852A1
; GENERAL INFORMATION:
;  APPLICANT: Dirk Petersohn
;  APPLICANT:  Kordula Schlotmann
;  APPLICANT:  Thomas Gassenmeier
;  APPLICANT:  Olaf Holtkotter
;  APPLICANT:  Marcus Conradt
;  APPLICANT:  Kay Hofmann
;  TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
;  FILE REFERENCE: H 05667 PCT
;  CURRENT APPLICATION NUMBER: US/11/158,209
;  CURRENT FILING DATE:  2005-06-20
;  PRIOR APPLICATION NUMBER: PCT/EP2003/014070
;  PRIOR FILING DATE: 2003-12-11
;  PRIOR APPLICATION NUMBER: 102 60 931.4-41
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 1335
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 545
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-158-209-545

  Query Match             49.4%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 6.6;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CAGCAACACT 12
              |||||| |||
Db         10 CAGCAAAACT 1


RESULT 7
US-11-212-812A-395
; Sequence 395, Application US/11212812A
; Publication No. US20060121452A1
; GENERAL INFORMATION:
;  APPLICANT: Dhallan, Ravinder S.
;  TITLE OF INVENTION: METHODS FOR DETECTION OF GENETIC
;  TITLE OF INVENTION:  DISORDERS
;  FILE REFERENCE: 543312000401
;  CURRENT APPLICATION NUMBER: US/11/212,812A
;  CURRENT FILING DATE:  2005-08-26
;  PRIOR APPLICATION NUMBER: PCT/US04/006337
;  PRIOR FILING DATE: 2004-03-01
;  PRIOR APPLICATION NUMBER: PCT/US03/06198
;  PRIOR FILING DATE: 2003-02-28
;  PRIOR APPLICATION NUMBER: US60/378,354
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;  PRIOR FILING DATE: 2002-05-08
;  NUMBER OF SEQ ID NOS: 725
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 395
;    LENGTH: 12
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Primer
US-11-212-812A-395

  Query Match             49.4%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 6.1;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TCAGCAACAC 11
              |||| |||||
Db          1 TCAGTAACAC 10


RESULT 8
US-11-212-386A-395
; Sequence 395, Application US/11212386A
; Publication No. US20060160105A1
; GENERAL INFORMATION:
;  APPLICANT: Dhallan, Ravinder S.
;  TITLE OF INVENTION: METHODS FOR DETECTION OF GENETIC
;  TITLE OF INVENTION:  DISORDERS
;  FILE REFERENCE: 543312000402
;  CURRENT APPLICATION NUMBER: US/11/212,386A
;  CURRENT FILING DATE:  2005-08-26
;  PRIOR APPLICATION NUMBER: US10/661,165
;  PRIOR FILING DATE: 2003-09-11
;  PRIOR APPLICATION NUMBER: PCT/US03/27308
;  PRIOR FILING DATE: 2003-08-29
;  PRIOR APPLICATION NUMBER: PCT/US03/06198
;  PRIOR FILING DATE: 2003-02-28
;  PRIOR APPLICATION NUMBER: US60/378,354
;  PRIOR FILING DATE: 2002-05-08
;  NUMBER OF SEQ ID NOS: 725
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 395
;    LENGTH: 12
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Primer
US-11-212-386A-395

  Query Match             49.4%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 6.1;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TCAGCAACAC 11
              |||| |||||
Db          1 TCAGTAACAC 10


RESULT 9
US-11-364-118-390/c
; Sequence 390, Application US/11364118
; Publication No. US20060204992A1
; GENERAL INFORMATION:
;  APPLICANT: Olaf Holtkotter
;  APPLICANT:  Dirk Petersohn
;  APPLICANT:  Kordula Schlotmann
;  APPLICANT:  Melanie Giesen
;  APPLICANT:  Daniela Kessler-Becker
;  TITLE OF INVENTION: Method for Determining Hair Cycle Markers
;  FILE REFERENCE: H 06059 PCT
;  CURRENT APPLICATION NUMBER: US/11/364,118
;  CURRENT FILING DATE:  2006-02-28
;  PRIOR APPLICATION NUMBER: PCT/EP2004/009435
;  PRIOR FILING DATE: 2004-08-24
;  PRIOR APPLICATION NUMBER: 103 40 373.6-41
;  PRIOR FILING DATE: 2003-08-30
;  NUMBER OF SEQ ID NOS: 570
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 390
;    LENGTH: 11
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-11-364-118-390

  Query Match             47.1%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 7.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 ACACTCCT 15
              ||||||||
Db          9 ACACTCCT 2


RESULT 10
US-11-364-118-457/c
; Sequence 457, Application US/11364118
; Publication No. US20060204992A1
; GENERAL INFORMATION:
;  APPLICANT: Olaf Holtkotter
;  APPLICANT:  Dirk Petersohn
;  APPLICANT:  Kordula Schlotmann
;  APPLICANT:  Melanie Giesen
;  APPLICANT:  Daniela Kessler-Becker
;  TITLE OF INVENTION: Method for Determining Hair Cycle Markers
;  FILE REFERENCE: H 06059 PCT
;  CURRENT APPLICATION NUMBER: US/11/364,118
;  CURRENT FILING DATE:  2006-02-28
;  PRIOR APPLICATION NUMBER: PCT/EP2004/009435
;  PRIOR FILING DATE: 2004-08-24
;  PRIOR APPLICATION NUMBER: 103 40 373.6-41
;  PRIOR FILING DATE: 2003-08-30
;  NUMBER OF SEQ ID NOS: 570
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 457
;    LENGTH: 11
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-11-364-118-457

  Query Match             47.1%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 7.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 ACACTCCT 15
              ||||||||
Db          9 ACACTCCT 2


RESULT 11
US-11-158-209-691/c
; Sequence 691, Application US/11158209
; Publication No. US20060088852A1
; GENERAL INFORMATION:
;  APPLICANT: Dirk Petersohn
;  APPLICANT:  Kordula Schlotmann
;  APPLICANT:  Thomas Gassenmeier
;  APPLICANT:  Olaf Holtkotter
;  APPLICANT:  Marcus Conradt
;  APPLICANT:  Kay Hofmann
;  TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
;  FILE REFERENCE: H 05667 PCT
;  CURRENT APPLICATION NUMBER: US/11/158,209
;  CURRENT FILING DATE:  2005-06-20
;  PRIOR APPLICATION NUMBER: PCT/EP2003/014070
;  PRIOR FILING DATE: 2003-12-11
;  PRIOR APPLICATION NUMBER: 102 60 931.4-41
```

```
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 1335
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 691
;    LENGTH: 11
;    TYPE: DNA
;    ORGANISM: Homo Sapiens
US-11-158-209-691

  Query Match             45.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 7.9;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 AGCAACACTCC 14
              |||  ||||||
Db         11 AGCTGCACTCC 1


RESULT 12
US-11-158-209-1221/c
; Sequence 1221, Application US/11158209
; Publication No. US20060088852A1
; GENERAL INFORMATION:
;  APPLICANT: Dirk Petersohn
;  APPLICANT:  Kordula Schlotmann
;  APPLICANT:  Thomas Gassenmeier
;  APPLICANT:  Olaf Holtkotter
;  APPLICANT:  Marcus Conradt
;  APPLICANT:  Kay Hofmann
;  TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
;  FILE REFERENCE: H 05667 PCT
;  CURRENT APPLICATION NUMBER: US/11/158,209
;  CURRENT FILING DATE:  2005-06-20
;  PRIOR APPLICATION NUMBER: PCT/EP2003/014070
;  PRIOR FILING DATE: 2003-12-11
;  PRIOR APPLICATION NUMBER: 102 60 931.4-41
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 1335
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 1221
;    LENGTH: 11
;    TYPE: DNA
;    ORGANISM: Homo Sapiens
US-11-158-209-1221

  Query Match             45.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 7.9;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACAC 11
              |||| | ||||
Db         11 CTCAACTACAC 1


RESULT 13
US-11-148-303-66
; Sequence 66, Application US/11148303
; Publication No. US20060154886A1
; GENERAL INFORMATION:
;  APPLICANT: Gruenenthal GmbH
;  TITLE OF INVENTION: Regulatory elements in the 5' region of the VR1 gene
;  FILE REFERENCE: GR01P003WO
;  CURRENT APPLICATION NUMBER: US/11/148,303
;  CURRENT FILING DATE:  2005-06-09
;  NUMBER OF SEQ ID NOS: 781
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
;    LENGTH: 11
;    TYPE: DNA
;    ORGANISM: Rattus norvegicus
;    FEATURE:
;    OTHER INFORMATION: V$NFY Q6
US-11-148-303-66

  Query Match             45.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 7.9;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TCAGCAACACT 12
              ||| ||| |||
Db          1 TCACCAATACT 11


RESULT 14
US-10-691-012-35/c
; Sequence 35, Application US/10691012
; Publication No. US20060160731A1
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: Peptide Nucleic Acids
;  FILE REFERENCE: ISIS0540
;  CURRENT APPLICATION NUMBER: US/10/691,012
;  CURRENT FILING DATE:  2003-10-22
;  PRIOR APPLICATION NUMBER: US/08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;    LENGTH: 10
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Novel Sequence
US-10-691-012-35

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 9.8;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 CACTCCTAT 17
              |||| ||||
Db         10 CACTACTAT 2


RESULT 15
US-11-148-303-23
; Sequence 23, Application US/11148303
; Publication No. US20060154886A1
; GENERAL INFORMATION:
;  APPLICANT: Gruenenthal GmbH
;  TITLE OF INVENTION: Regulatory elements in the 5' region of the VR1 gene
;  FILE REFERENCE: GR01P003WO
;  CURRENT APPLICATION NUMBER: US/11/148,303
;  CURRENT FILING DATE:  2005-06-09
;  NUMBER OF SEQ ID NOS: 781
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
;    LENGTH: 10
;    TYPE: DNA
;    ORGANISM: Rattus norvegicus
;    FEATURE:
;    OTHER INFORMATION: V$SOX5 01
US-11-148-303-23

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 9.8;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCC 14
              ||||| |||
Db          2 CAACAATCC 10
```

```
RESULT 16
US-11-148-303-128
; Sequence 128, Application US/11148303
; Publication No. US20060154886A1
; GENERAL INFORMATION:
;  APPLICANT: Gruenenthal GmbH
;  TITLE OF INVENTION: Regulatory elements in the 5' region of the VR1 gene
;  FILE REFERENCE: GR01P003WO
;  CURRENT APPLICATION NUMBER: US/11/148,303
;  CURRENT FILING DATE:  2005-06-09
;  NUMBER OF SEQ ID NOS: 781
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 128
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   OTHER INFORMATION: V$SOX5 01
US-11-148-303-128

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 9.8;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GCAACACTC 13
              |||||| ||
Db          1 GCAACAATC 9


Search completed: November 21, 2006, 14:33:58
Job time : 0.001 secs
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2006, 14:32:49 ; Search time 0.001 Seconds
(without alignments)
117.640 Million cell updates/sec

Title: US-10-823-197-7
Perfect score: 17
Sequence: 1 CTCAGCAACACTCCTAT 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 262 seqs, 3460 residues

Total number of hits satisfying chosen parameters: 524

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 262 summaries

Database : rnpbmdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	17	100.0	17	1	US-09-845-129-22	Sequence 22, Appl
	2	17	100.0	17	1	US-09-888-056A-3	Sequence 3, Appli
	3	17	100.0	17	1	US-10-167-127-23	Sequence 23, Appl
	4	17	100.0	17	1	US-10-172-919-7	Sequence 7, Appli
	5	17	100.0	17	1	US-10-320-360-1	Sequence 1, Appli
	6	17	100.0	17	1	US-10-802-061-22	Sequence 22, Appl
	7	17	100.0	17	1	US-10-823-197-7	Sequence 7, Appli
	8	17	100.0	17	1	US-10-712-882-5	Sequence 5, Appli
	9	17	100.0	17	1	US-10-838-503-9	Sequence 9, Appli
	10	17	100.0	17	1	US-11-121-634-22	Sequence 22, Appl
	11	14	82.4	17	1	US-10-626-830-9	Sequence 9, Appli
c	12	14	82.4	19	1	US-11-083-784-1215680	Sequence 1215680,
c	13	14	82.4	19	1	US-11-083-784-1215694	Sequence 1215694,
c	14	14	82.4	19	1	US-11-083-784-1215717	Sequence 1215717,
c	15	14	82.4	19	1	US-11-101-244-1215680	Sequence 1215680,
c	16	14	82.4	19	1	US-11-101-244-1215694	Sequence 1215694,
c	17	14	82.4	19	1	US-11-101-244-1215717	Sequence 1215717,
c	18	13.8	81.2	19	1	US-10-310-914A-273328	Sequence 273328,
	19	13.8	81.2	19	1	US-11-083-784-921461	Sequence 921461,
c	20	13.8	81.2	19	1	US-11-083-784-1372880	Sequence 1372880,
	21	13.8	81.2	19	1	US-11-101-244-921461	Sequence 921461,
c	22	13.8	81.2	19	1	US-11-101-244-1372880	Sequence 1372880,
c	23	13.4	78.8	19	1	US-11-083-784-628637	Sequence 628637,
c	24	13.4	78.8	19	1	US-11-083-784-628845	Sequence 628845,
c	25	13.4	78.8	19	1	US-11-101-244-628637	Sequence 628637,
c	26	13.4	78.8	19	1	US-11-101-244-628845	Sequence 628845,
c	27	12.8	75.3	18	1	US-10-310-914A-273305	Sequence 273305,
c	28	12.4	72.9	16	1	US-10-096-125-14	Sequence 14, Appl
c	29	11	64.7	12	1	US-10-257-017B-302368	Sequence 302368,
c	30	11	64.7	13	1	US-10-257-017B-71093	Sequence 71093, A
	31	11	64.7	13	1	US-10-257-017B-71094	Sequence 71094, A
c	32	11	64.7	13	1	US-10-257-017B-136017	Sequence 136017,
	33	11	64.7	13	1	US-10-257-017B-136018	Sequence 136018,
	34	10.8	63.5	15	1	US-09-848-754A-9312	Sequence 9312, Ap
c	35	10.4	61.2	12	1	US-10-257-017B-290676	Sequence 290676,
c	36	10.4	61.2	12	1	US-10-257-017B-359911	Sequence 359911,
c	37	10.4	61.2	13	1	US-10-257-017B-51767	Sequence 51767, A
	38	10.4	61.2	13	1	US-10-257-017B-51768	Sequence 51768, A
c	39	10.4	61.2	13	1	US-10-257-017B-159811	Sequence 159811,
	40	10.4	61.2	13	1	US-10-257-017B-159812	Sequence 159812,
c	41	10.4	61.2	13	1	US-10-257-017B-163329	Sequence 163329,
	42	10.4	61.2	13	1	US-10-257-017B-163330	Sequence 163330,
c	43	10.4	61.2	13	1	US-10-257-017B-179987	Sequence 179987,
	44	10.4	61.2	13	1	US-10-257-017B-179988	Sequence 179988,
c	45	10.4	61.2	13	1	US-10-257-017B-191043	Sequence 191043,
	46	10.4	61.2	13	1	US-10-257-017B-191044	Sequence 191044,
c	47	10.4	61.2	13	1	US-10-257-017B-222887	Sequence 222887,
	48	10.4	61.2	13	1	US-10-257-017B-222888	Sequence 222888,
c	49	10.4	61.2	13	1	US-10-257-017B-223803	Sequence 223803,
	50	10.4	61.2	13	1	US-10-257-017B-223804	Sequence 223804,
c	51	10.4	61.2	13	1	US-10-257-017B-251633	Sequence 251633,
	52	10.4	61.2	13	1	US-10-257-017B-251634	Sequence 251634,
c	53	10.4	61.2	13	1	US-10-257-017B-262259	Sequence 262259,
	54	10.4	61.2	13	1	US-10-257-017B-262260	Sequence 262260,
c	55	10	58.8	10	1	US-10-078-958-42	Sequence 42, Appl
	56	10	58.8	12	1	US-10-257-017B-280408	Sequence 280408,
	57	10	58.8	12	1	US-10-257-017B-321905	Sequence 321905,
c	58	10	58.8	12	1	US-10-257-017B-331426	Sequence 331426,
c	59	10	58.8	12	1	US-10-257-017B-338789	Sequence 338789,
	60	10	58.8	12	1	US-10-257-017B-352664	Sequence 352664,
	61	10	58.8	12	1	US-10-257-017B-360235	Sequence 360235,
c	62	10	58.8	12	1	US-10-257-017B-375248	Sequence 375248,
	63	10	58.8	12	1	US-10-257-017B-381603	Sequence 381603,
c	64	10	58.8	13	1	US-10-257-017B-14333	Sequence 14333, A
	65	10	58.8	13	1	US-10-257-017B-14334	Sequence 14334, A
c	66	10	58.8	13	1	US-10-257-017B-55559	Sequence 55559, A
	67	10	58.8	13	1	US-10-257-017B-55560	Sequence 55560, A
c	68	10	58.8	13	1	US-10-257-017B-56319	Sequence 56319, A
	69	10	58.8	13	1	US-10-257-017B-56320	Sequence 56320, A
c	70	10	58.8	13	1	US-10-257-017B-56321	Sequence 56321, A
	71	10	58.8	13	1	US-10-257-017B-56322	Sequence 56322, A
c	72	10	58.8	13	1	US-10-257-017B-118021	Sequence 118021,
	73	10	58.8	13	1	US-10-257-017B-118022	Sequence 118022,
c	74	10	58.8	13	1	US-10-257-017B-227361	Sequence 227361,
	75	10	58.8	13	1	US-10-257-017B-227362	Sequence 227362,
c	76	10	58.8	13	1	US-10-257-017B-242737	Sequence 242737,
	77	10	58.8	13	1	US-10-257-017B-242738	Sequence 242738,
c	78	9.8	57.6	13	1	US-10-257-017B-47179	Sequence 47179, A
	79	9.8	57.6	13	1	US-10-257-017B-47180	Sequence 47180, A
c	80	9.8	57.6	13	1	US-10-257-017B-106893	Sequence 106893,
	81	9.8	57.6	13	1	US-10-257-017B-106894	Sequence 106894,
c	82	9.8	57.6	13	1	US-10-257-017B-110493	Sequence 110493,
	83	9.8	57.6	13	1	US-10-257-017B-110494	Sequence 110494,
c	84	9.8	57.6	13	1	US-10-257-017B-120667	Sequence 120667,
	85	9.8	57.6	13	1	US-10-257-017B-120668	Sequence 120668,
c	86	9.8	57.6	13	1	US-10-257-017B-123899	Sequence 123899,
	87	9.8	57.6	13	1	US-10-257-017B-123900	Sequence 123900,
c	88	9.8	57.6	13	1	US-10-257-017B-174605	Sequence 174605,
	89	9.8	57.6	13	1	US-10-257-017B-174606	Sequence 174606,
c	90	9.8	57.6	13	1	US-10-257-017B-209793	Sequence 209793,
	91	9.8	57.6	13	1	US-10-257-017B-209794	Sequence 209794,
c	92	9.8	57.6	13	1	US-10-257-017B-246251	Sequence 246251,
	93	9.8	57.6	13	1	US-10-257-017B-246252	Sequence 246252,
c	94	9.6	56.5	13	1	US-10-257-017B-1985	Sequence 1985, Ap
	95	9.6	56.5	13	1	US-10-257-017B-1986	Sequence 1986, Ap
c	96	9.6	56.5	13	1	US-10-257-017B-194753	Sequence 194753,
	97	9.6	56.5	13	1	US-10-257-017B-194754	Sequence 194754,
c	98	9.4	55.3	11	1	US-10-450-797-527	Sequence 527, App
	99	9.4	55.3	12	1	US-10-257-017B-272469	Sequence 272469,
c	100	9.4	55.3	12	1	US-10-257-017B-280007	Sequence 280007,
	101	9.4	55.3	12	1	US-10-257-017B-282853	Sequence 282853,
	102	9.4	55.3	12	1	US-10-257-017B-283403	Sequence 283403,
c	103	9.4	55.3	12	1	US-10-257-017B-285422	Sequence 285422,
c	104	9.4	55.3	12	1	US-10-257-017B-287174	Sequence 287174,
	105	9.4	55.3	12	1	US-10-257-017B-313510	Sequence 313510,
	106	9.4	55.3	12	1	US-10-257-017B-315837	Sequence 315837,

107	9.4	55.3	12	1	US-10-257-017B-321267	Sequence 321267,
c 108	9.4	55.3	12	1	US-10-257-017B-321352	Sequence 321352,
c 109	9.4	55.3	12	1	US-10-257-017B-327218	Sequence 327218,
c 110	9.4	55.3	12	1	US-10-257-017B-332452	Sequence 332452,
c 111	9.4	55.3	12	1	US-10-257-017B-337997	Sequence 337997,
112	9.4	55.3	12	1	US-10-257-017B-351387	Sequence 351387,
113	9.4	55.3	12	1	US-10-257-017B-359454	Sequence 359454,
114	9.4	55.3	12	1	US-10-257-017B-369661	Sequence 369661,
115	9.4	55.3	12	1	US-10-257-017B-370250	Sequence 370250,
c 116	9.4	55.3	12	1	US-10-257-017B-379229	Sequence 379229,
c 117	9.4	55.3	12	1	US-10-257-017B-379316	Sequence 379316,
c 118	9.4	55.3	13	1	US-10-257-017B-309	Sequence 309, App
119	9.4	55.3	13	1	US-10-257-017B-310	Sequence 310, App
c 120	9.4	55.3	13	1	US-10-257-017B-24595	Sequence 24595, A
121	9.4	55.3	13	1	US-10-257-017B-24596	Sequence 24596, A
c 122	9.4	55.3	13	1	US-10-257-017B-25817	Sequence 25817, A
123	9.4	55.3	13	1	US-10-257-017B-25818	Sequence 25818, A
c 124	9.4	55.3	13	1	US-10-257-017B-39645	Sequence 39645, A
125	9.4	55.3	13	1	US-10-257-017B-39646	Sequence 39646, A
c 126	9.4	55.3	13	1	US-10-257-017B-42741	Sequence 42741, A
127	9.4	55.3	13	1	US-10-257-017B-42742	Sequence 42742, A
c 128	9.4	55.3	13	1	US-10-257-017B-47389	Sequence 47389, A
129	9.4	55.3	13	1	US-10-257-017B-47390	Sequence 47390, A
c 130	9.4	55.3	13	1	US-10-257-017B-50897	Sequence 50897, A
131	9.4	55.3	13	1	US-10-257-017B-50898	Sequence 50898, A
c 132	9.4	55.3	13	1	US-10-257-017B-62449	Sequence 62449, A
133	9.4	55.3	13	1	US-10-257-017B-62450	Sequence 62450, A
c 134	9.4	55.3	13	1	US-10-257-017B-71091	Sequence 71091, A
135	9.4	55.3	13	1	US-10-257-017B-71092	Sequence 71092, A
c 136	9.4	55.3	13	1	US-10-257-017B-71097	Sequence 71097, A
137	9.4	55.3	13	1	US-10-257-017B-71098	Sequence 71098, A
c 138	9.4	55.3	13	1	US-10-257-017B-71101	Sequence 71101, A
139	9.4	55.3	13	1	US-10-257-017B-71102	Sequence 71102, A
c 140	9.4	55.3	13	1	US-10-257-017B-75403	Sequence 75403, A
141	9.4	55.3	13	1	US-10-257-017B-75404	Sequence 75404, A
c 142	9.4	55.3	13	1	US-10-257-017B-78917	Sequence 78917, A
143	9.4	55.3	13	1	US-10-257-017B-78918	Sequence 78918, A
c 144	9.4	55.3	13	1	US-10-257-017B-86481	Sequence 86481, A
145	9.4	55.3	13	1	US-10-257-017B-86482	Sequence 86482, A
c 146	9.4	55.3	13	1	US-10-257-017B-86483	Sequence 86483, A
147	9.4	55.3	13	1	US-10-257-017B-86484	Sequence 86484, A
c 148	9.4	55.3	13	1	US-10-257-017B-96645	Sequence 96645, A
149	9.4	55.3	13	1	US-10-257-017B-96646	Sequence 96646, A
c 150	9.4	55.3	13	1	US-10-257-017B-104399	Sequence 104399,
151	9.4	55.3	13	1	US-10-257-017B-104400	Sequence 104400,
c 152	9.4	55.3	13	1	US-10-257-017B-108233	Sequence 108233,
153	9.4	55.3	13	1	US-10-257-017B-108234	Sequence 108234,
c 154	9.4	55.3	13	1	US-10-257-017B-111807	Sequence 111807,
155	9.4	55.3	13	1	US-10-257-017B-111808	Sequence 111808,
c 156	9.4	55.3	13	1	US-10-257-017B-117651	Sequence 117651,
157	9.4	55.3	13	1	US-10-257-017B-117652	Sequence 117652,
c 158	9.4	55.3	13	1	US-10-257-017B-127381	Sequence 127381,
159	9.4	55.3	13	1	US-10-257-017B-127382	Sequence 127382,
c 160	9.4	55.3	13	1	US-10-257-017B-127385	Sequence 127385,
161	9.4	55.3	13	1	US-10-257-017B-127386	Sequence 127386,
c 162	9.4	55.3	13	1	US-10-257-017B-132701	Sequence 132701,
163	9.4	55.3	13	1	US-10-257-017B-132702	Sequence 132702,
c 164	9.4	55.3	13	1	US-10-257-017B-136015	Sequence 136015,
165	9.4	55.3	13	1	US-10-257-017B-136016	Sequence 136016,
c 166	9.4	55.3	13	1	US-10-257-017B-153289	Sequence 153289,
167	9.4	55.3	13	1	US-10-257-017B-153290	Sequence 153290,
c 168	9.4	55.3	13	1	US-10-257-017B-153995	Sequence 153995,
169	9.4	55.3	13	1	US-10-257-017B-153996	Sequence 153996,
c 170	9.4	55.3	13	1	US-10-257-017B-157065	Sequence 157065,
171	9.4	55.3	13	1	US-10-257-017B-157066	Sequence 157066,
c 172	9.4	55.3	13	1	US-10-257-017B-169365	Sequence 169365,
173	9.4	55.3	13	1	US-10-257-017B-169366	Sequence 169366,
c 174	9.4	55.3	13	1	US-10-257-017B-173017	Sequence 173017,
175	9.4	55.3	13	1	US-10-257-017B-173018	Sequence 173018,
c 176	9.4	55.3	13	1	US-10-257-017B-174909	Sequence 174909,
177	9.4	55.3	13	1	US-10-257-017B-174910	Sequence 174910,
c 178	9.4	55.3	13	1	US-10-257-017B-175703	Sequence 175703,
179	9.4	55.3	13	1	US-10-257-017B-175704	Sequence 175704,
c 180	9.4	55.3	13	1	US-10-257-017B-178081	Sequence 178081,
181	9.4	55.3	13	1	US-10-257-017B-178082	Sequence 178082,
c 182	9.4	55.3	13	1	US-10-257-017B-179041	Sequence 179041,
183	9.4	55.3	13	1	US-10-257-017B-179042	Sequence 179042,
c 184	9.4	55.3	13	1	US-10-257-017B-190349	Sequence 190349,
185	9.4	55.3	13	1	US-10-257-017B-190350	Sequence 190350,
c 186	9.4	55.3	13	1	US-10-257-017B-200109	Sequence 200109,
187	9.4	55.3	13	1	US-10-257-017B-200110	Sequence 200110,
c 188	9.4	55.3	13	1	US-10-257-017B-207959	Sequence 207959,
189	9.4	55.3	13	1	US-10-257-017B-207960	Sequence 207960,
c 190	9.4	55.3	13	1	US-10-257-017B-211433	Sequence 211433,
191	9.4	55.3	13	1	US-10-257-017B-211434	Sequence 211434,
c 192	9.4	55.3	13	1	US-10-257-017B-226549	Sequence 226549,
193	9.4	55.3	13	1	US-10-257-017B-226550	Sequence 226550,
c 194	9.4	55.3	13	1	US-10-257-017B-227085	Sequence 227085,
195	9.4	55.3	13	1	US-10-257-017B-227086	Sequence 227086,
c 196	9.4	55.3	13	1	US-10-257-017B-227087	Sequence 227087,
197	9.4	55.3	13	1	US-10-257-017B-227088	Sequence 227088,
c 198	9.4	55.3	13	1	US-10-257-017B-233119	Sequence 233119,
199	9.4	55.3	13	1	US-10-257-017B-233120	Sequence 233120,
c 200	9.4	55.3	13	1	US-10-257-017B-233225	Sequence 233225,
201	9.4	55.3	13	1	US-10-257-017B-233226	Sequence 233226,
c 202	9.4	55.3	13	1	US-10-257-017B-235003	Sequence 235003,
203	9.4	55.3	13	1	US-10-257-017B-235004	Sequence 235004,
c 204	9.4	55.3	13	1	US-10-257-017B-248677	Sequence 248677,
205	9.4	55.3	13	1	US-10-257-017B-248678	Sequence 248678,
c 206	9.4	55.3	13	1	US-10-257-017B-259087	Sequence 259087,
207	9.4	55.3	13	1	US-10-257-017B-259088	Sequence 259088,
c 208	9.4	55.3	13	1	US-10-257-017B-263309	Sequence 263309,
209	9.4	55.3	13	1	US-10-257-017B-263310	Sequence 263310,
c 210	9	52.9	11	1	US-09-249-155-146	Sequence 146, App
c 211	9	52.9	11	1	US-10-314-322-146	Sequence 146, App
212	9	52.9	12	1	US-10-257-017B-274536	Sequence 274536,
213	9	52.9	12	1	US-10-257-017B-289056	Sequence 289056,
214	9	52.9	12	1	US-10-257-017B-304514	Sequence 304514,
c 215	9	52.9	12	1	US-10-257-017B-308500	Sequence 308500,
216	9	52.9	12	1	US-10-257-017B-309034	Sequence 309034,
217	9	52.9	12	1	US-10-257-017B-318085	Sequence 318085,
c 218	9	52.9	12	1	US-10-257-017B-318464	Sequence 318464,
c 219	9	52.9	12	1	US-10-257-017B-331427	Sequence 331427,
220	9	52.9	12	1	US-10-257-017B-336064	Sequence 336064,
221	9	52.9	12	1	US-10-257-017B-349259	Sequence 349259,
c 222	9	52.9	12	1	US-10-257-017B-351084	Sequence 351084,
223	9	52.9	12	1	US-10-257-017B-352964	Sequence 352964,
224	8.8	51.8	12	1	US-10-257-017B-270123	Sequence 270123,
225	8.8	51.8	12	1	US-10-257-017B-271995	Sequence 271995,
226	8.8	51.8	12	1	US-10-257-017B-277739	Sequence 277739,
c 227	8.8	51.8	12	1	US-10-257-017B-282732	Sequence 282732,
228	8.8	51.8	12	1	US-10-257-017B-289048	Sequence 289048,
229	8.8	51.8	12	1	US-10-257-017B-290054	Sequence 290054,
230	8.8	51.8	12	1	US-10-257-017B-290876	Sequence 290876,
231	8.8	51.8	12	1	US-10-257-017B-295767	Sequence 295767,
232	8.8	51.8	12	1	US-10-257-017B-298432	Sequence 298432,
c 233	8.8	51.8	12	1	US-10-257-017B-303022	Sequence 303022,
234	8.8	51.8	12	1	US-10-257-017B-307432	Sequence 307432,
c 235	8.8	51.8	12	1	US-10-257-017B-307496	Sequence 307496,
c 236	8.8	51.8	12	1	US-10-257-017B-313414	Sequence 313414,
237	8.8	51.8	12	1	US-10-257-017B-314086	Sequence 314086,
238	8.8	51.8	12	1	US-10-257-017B-314087	Sequence 314087,
239	8.8	51.8	12	1	US-10-257-017B-321092	Sequence 321092,
240	8.8	51.8	12	1	US-10-257-017B-321102	Sequence 321102,
241	8.8	51.8	12	1	US-10-257-017B-322014	Sequence 322014,
242	8.8	51.8	12	1	US-10-257-017B-322790	Sequence 322790,
c 243	8.8	51.8	12	1	US-10-257-017B-326438	Sequence 326438,
244	8.8	51.8	12	1	US-10-257-017B-328173	Sequence 328173,
c 245	8.8	51.8	12	1	US-10-257-017B-329594	Sequence 329594,
c 246	8.8	51.8	12	1	US-10-257-017B-332773	Sequence 332773,
247	8.8	51.8	12	1	US-10-257-017B-343778	Sequence 343778,
248	8.8	51.8	12	1	US-10-257-017B-351291	Sequence 351291,
249	8.8	51.8	12	1	US-10-257-017B-352679	Sequence 352679,
250	8.8	51.8	12	1	US-10-257-017B-352697	Sequence 352697,
c 251	8.8	51.8	12	1	US-10-257-017B-353232	Sequence 353232,
c 252	8.8	51.8	12	1	US-10-257-017B-357288	Sequence 357288,

c 253	8.8	51.8	12	1	US-10-257-017B-360500	Sequence 360500,
c 254	8.8	51.8	12	1	US-10-257-017B-362463	Sequence 362463,
c 255	8.8	51.8	12	1	US-10-257-017B-367935	Sequence 367935,
256	8.8	51.8	12	1	US-10-257-017B-369135	Sequence 369135,
c 257	8.8	51.8	12	1	US-10-257-017B-370100	Sequence 370100,
c 258	8.8	51.8	12	1	US-10-257-017B-371753	Sequence 371753,
c 259	8.8	51.8	12	1	US-10-257-017B-374492	Sequence 374492,
260	8.8	51.8	12	1	US-10-257-017B-375813	Sequence 375813,
c 261	8.8	51.8	12	1	US-10-257-017B-379818	Sequence 379818,
262	8.8	51.8	12	1	US-10-257-017B-379853	Sequence 379853,

ALIGNMENTS

RESULT 1
US-09-845-129-22
; Sequence 22, Application US/09845129
; Patent No. US20020146700A1
; GENERAL INFORMATION:
; APPLICANT: DUFF, GORDON W.
; APPLICANT: COX, ANGELA
; APPLICANT: CAMP, NICOLA J.
; APPLICANT: DIGIOVINE, FRANCESCO S.
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH AN IL-1 INFLAMMATORY HAPLOTYPE
; FILE REFERENCE: MSA-010.02
; CURRENT APPLICATION NUMBER: US/09/845,129
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 09/345,217
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: PCT/GB98/01481
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 9711040.7
; PRIOR FILING DATE: 1997-05-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-845-129-22

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
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Db 1 CTCAGCAACACTCCTAT 17

RESULT 2
US-09-888-056A-3
; Sequence 3, Application US/09888056A
; Publication No. US20030124524A1
; GENERAL INFORMATION:
; APPLICANT: KORNMAN, KENNETH S.
; APPLICANT: DUFF, GORDON W.
; TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING MODULATORS OF THE
; TITLE OF INVENTION: INFLAMAMTORY OR IMMUNE RESPONSE
; FILE REFERENCE: MSA-023.01
; CURRENT APPLICATION NUMBER: US/09/888,056A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/213,853
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-888-056A-3

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
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Db 1 CTCAGCAACACTCCTAT 17

RESULT 3
US-10-167-127-23
; Sequence 23, Application US/10167127
; Publication No. US20030100031A1
; GENERAL INFORMATION:
; APPLICANT: DOWER, STEVEN
; APPLICANT: DUFF, GORDON W.
; TITLE OF INVENTION: INTEGRATIVE ASSAYS FOR MONITORING MOLECULAR ASSEMBLY
; TITLE OF INVENTION: EVENTS
; FILE REFERENCE: MSA-026.01 (20974-2601)
; CURRENT APPLICATION NUMBER: US/10/167,127
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 60/297,305
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-167-127-23

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAACACTCCTAT 17
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Db 1 CTCAGCAACACTCCTAT 17

RESULT 4
US-10-172-919-7
; Sequence 7, Application US/10172919
; Publication No. US20030152947A1
; GENERAL INFORMATION:
; APPLICANT: CROSSMAN, DAVID C.
; APPLICANT: DUFF, GORDON W.
; APPLICANT: FRANCIS, SHEILA E.
; APPLICANT: KORNMAN, KENNETH S.
; APPLICANT: BARNETT, KATHERINE
; TITLE OF INVENTION: METHODS FOR DETECTING AND TREATING THE EARLY ONSET OF
; TITLE OF INVENTION: AGING-RELATED CONDITIONS
; FILE REFERENCE: MSA-025.01
; CURRENT APPLICATION NUMBER: US/10/172,919
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/298,493
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-172-919-7

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  Best Local Similarity  100.0%;  Pred. No. 14;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 CTCAGCAACACTCCTAT 17


RESULT 5
US-10-320-360-1
; Sequence 1, Application US/10320360
; Publication No. US20030175764A1
; GENERAL INFORMATION:
;  APPLICANT: Francis, Sheila E.
;  APPLICANT:  Crossman, David C.
;  APPLICANT:  Duff, Gordon W.
;  APPLICANT:  Kornman, Kenneth S.
;  APPLICANT:  Stephenson, Katherine
;  TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR CARDIOVASCULAR
;  TITLE OF INVENTION:  DISORDERS
;  FILE REFERENCE: MSA-006.03
;  CURRENT APPLICATION NUMBER: US/10/320,360
;  CURRENT FILING DATE:  2002-12-13
;  PRIOR APPLICATION NUMBER: 09/320,395
;  PRIOR FILING DATE: 1999-05-26
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-320-360-1

  Query Match           100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 14;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 6
US-10-802-061-22
; Sequence 22, Application US/10802061
; Publication No. US20040152124A1
; GENERAL INFORMATION:
;  APPLICANT: DUFF, GORDON W.
;  APPLICANT:  COX, ANGELA
;  APPLICANT:  CAMP, NICOLA J.
;  APPLICANT:  DIGIOVINE, FRANCESCO S.
;  TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR DISEASES ASSOCIATED
;  TITLE OF INVENTION:  WITH AN IL-1 INFLAMMATORY HAPLOTYPE
;  FILE REFERENCE: 24299-508CON3
;  CURRENT APPLICATION NUMBER: US/10/802,061
;  CURRENT FILING DATE:  2004-03-15
;  PRIOR APPLICATION NUMBER: 09/845,129
;  PRIOR FILING DATE: 2001-04-27
;  PRIOR APPLICATION NUMBER: 09/345,217
;  PRIOR FILING DATE: 1999-06-30
;  PRIOR APPLICATION NUMBER: PCT/GB98/01481
;  PRIOR FILING DATE: 1998-05-21
;  PRIOR APPLICATION NUMBER: 9711040.7
;  PRIOR FILING DATE: 1997-05-29
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-802-061-22

  Query Match           100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 14;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 7
US-10-823-197-7
; Sequence 7, Application US/10823197
; Publication No. US20040229264A1
; GENERAL INFORMATION:
;  APPLICANT: CROSSMAN, DAVID C.
;  APPLICANT:  DUFF, GORDON W.
;  APPLICANT:  FRANCIS, SHEILA E.
;  APPLICANT:  KORNMAN, KENNETH S.
;  APPLICANT:  STEPHENSON, KATHERINE
;  TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR RESTENOSIS
;  FILE REFERENCE: 24299-514CIP2A DIV
;  CURRENT APPLICATION NUMBER: US/10/823,197
;  CURRENT FILING DATE:  2004-04-12
;  PRIOR APPLICATION NUMBER: 09/578,534
;  PRIOR FILING DATE: 2000-05-24
;  PRIOR APPLICATION NUMBER: 09/431,352
;  PRIOR FILING DATE: 1999-11-01
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-823-197-7

  Query Match           100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 14;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 8
US-10-712-882-5
; Sequence 5, Application US/10712882
; Publication No. US20050032077A1
;   GENERAL INFORMATION:
;        APPLICANT: Duff, Gordon W.
;                   Richardson, Robert R.S.
;                   Rennie, Ian G.
;        TITLE OF INVENTION: DETECTING GENETIC PREDISPOSITION TO
;                            SIGHT-THREATENING DIABETIC RETINOPATHY
;        NUMBER OF SEQUENCES: 10
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FOLEY, HOAG & ELIOT LLP
;             STREET: One Post Office Square
;             CITY: Boston
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02109-2170
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/712,882
;           FILING DATE: 12-Nov-2003
;           CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US/09/037,472
;           FILING DATE: 10-MAR-1998
;           APPLICATION NUMBER: PCT/GB97/02790
;           FILING DATE: 09-OCT-1997
;       ATTORNEY/AGENT INFORMATION:
;           NAME: Arnold, Beth E.
;           REGISTRATION NUMBER: 35,430
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (617) 832-1000
;           TELEFAX: (617) 832-7000
;   INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 17 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;           DESCRIPTION: /desc = "primer"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-712-882-5

  Query Match           100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 14;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 9
US-10-838-503-9
; Sequence 9, Application US/10838503
; Publication No. US20050064453A1
; GENERAL INFORMATION:
;  APPLICANT: DUFF, GORDON
;  APPLICANT:  KORNMAN, KENNETH
;  APPLICANT:  VAN DIJK, SIMON
;  TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR EARLY-ONSET MENOPAUSE
;  FILE REFERENCE: MSA-012.01
;  CURRENT APPLICATION NUMBER: US/10/838,503
;  CURRENT FILING DATE:  2004-05-03
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-10-838-503-9

  Query Match           100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 14;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 10
US-11-121-634-22
; Sequence 22, Application US/11121634
; Publication No. US20050282198A1
; GENERAL INFORMATION:
;  APPLICANT: Duff, Gordon
;  TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with an IL-1
;  TITLE OF INVENTION:  Inflammatory Haplotype
;  FILE REFERENCE: 24299-508CON3 CIP1
;  CURRENT APPLICATION NUMBER: US/11/121,634
;  CURRENT FILING DATE:  2005-05-03
;  PRIOR APPLICATION NUMBER: US 10/802,061
;  PRIOR FILING DATE: 2004-03-15
;  PRIOR APPLICATION NUMBER: US 09/845,129
;  PRIOR FILING DATE: 2001-04-27
;  PRIOR APPLICATION NUMBER: US 09/345,217
;  PRIOR FILING DATE: 1999-06-30
;  PRIOR APPLICATION NUMBER: PCT/GB98/01481
;  PRIOR FILING DATE: 1998-05-21
;  PRIOR APPLICATION NUMBER: GB9711040.7
;  PRIOR FILING DATE: 1997-05-29
;  PRIOR APPLICATION NUMBER: US 10/300,011
;  PRIOR FILING DATE: 2002-11-19
;  PRIOR APPLICATION NUMBER: US 60/386,020
;  PRIOR FILING DATE: 2002-06-05
;  PRIOR APPLICATION NUMBER: US 60/331,681
;  PRIOR FILING DATE: 2001-11-19
;  PRIOR APPLICATION NUMBER: US 60/567,727
;  PRIOR FILING DATE: 2004-05-03
;  NUMBER OF SEQ ID NOS: 202
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized primer
US-11-121-634-22

  Query Match           100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 14;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 11
US-10-626-830-9
; Sequence 9, Application US/10626830
; Publication No. US20040229228A1
; GENERAL INFORMATION:
;  APPLICANT: Sims, John E.
;  APPLICANT:  Kaufman, Dixon B.
;  TITLE OF INVENTION: IL-1 Genotype in Early Kidney Allograft Rejection
;  FILE REFERENCE: NWESTERN-08309
;  CURRENT APPLICATION NUMBER: US/10/626,830
;  CURRENT FILING DATE:  2003-07-24
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-626-830-9

  Query Match            82.4%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 35;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCC 14
              ||||||||||||||
Db          4 CTCAGCAACACTCC 17
```

```
RESULT 12
US-11-083-784-1215680/c
; Sequence 1215680, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1215680
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1215680

  Query Match             82.4%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 39;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CAGCAACACTCCTA 16
              ||||||||||||||
Db         16 CAGCAACACTCCTA 3


RESULT 13
US-11-083-784-1215694/c
; Sequence 1215694, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1215694
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1215694

  Query Match             82.4%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 39;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CAGCAACACTCCTA 16
              ||||||||||||||
Db         15 CAGCAACACTCCTA 2


RESULT 14
US-11-083-784-1215717/c
; Sequence 1215717, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1215717
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1215717

  Query Match             82.4%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 39;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CAGCAACACTCCTA 16
              ||||||||||||||
Db         17 CAGCAACACTCCTA 4


RESULT 15
US-11-101-244-1215680/c
; Sequence 1215680, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1215680
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-1215680

  Query Match             82.4%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 39;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CAGCAACACTCCTA 16
```

```
                ||||||||||||||
Db         16 CAGCAACACTCCTA 3


RESULT 16
US-11-101-244-1215694/c
; Sequence 1215694, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1215694
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-1215694

  Query Match             82.4%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 39;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CAGCAACACTCCTA 16
              ||||||||||||||
Db         15 CAGCAACACTCCTA 2


RESULT 17
US-11-101-244-1215717/c
; Sequence 1215717, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1215717
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-1215717

  Query Match             82.4%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 39;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CAGCAACACTCCTA 16
              ||||||||||||||
Db         17 CAGCAACACTCCTA 4


RESULT 18
US-10-310-914A-273328/c
; Sequence 273328, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 273328
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-273328

  Query Match             81.2%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 42;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              | ||||||| |||||||
Db         19 CCCAGCAACCCTCCTAT 3


RESULT 19
US-11-083-784-921461
; Sequence 921461, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 921461
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-921461

  Query Match             81.2%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   64.7%;  Pred. No. 42;
  Matches   11;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |:||||| | |:||:|:
Db          1 CUCAGCAUCUCUCCUAU 17


RESULT 20
US-11-083-784-1372880/c
; Sequence 1372880, Application US/11083784
```

```
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1372880
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1372880

  Query Match             81.2%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 42;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||| | ||||||||||
Db         19 CTCAACTACACTCCTAT 3


RESULT 21
US-11-101-244-921461
; Sequence 921461, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 921461
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-921461

  Query Match             81.2%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   64.7%;  Pred. No. 42;
  Matches   11;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |:||||| | |:||:|:
Db          1 CUCAGCAUCUCUCCUAU 17


RESULT 22
US-11-101-244-1372880/c
; Sequence 1372880, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1372880
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-1372880

  Query Match             81.2%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 42;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||| | ||||||||||
Db         19 CTCAACTACACTCCTAT 3


RESULT 23
US-11-083-784-628637/c
; Sequence 628637, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 628637
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-628637

  Query Match             78.8%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 47;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCT 15
              ||||| |||||||||
Db         18 CTCAGAAACACTCCT 4


RESULT 24
```

```
US-11-083-784-628845/c
; Sequence 628845, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 628845
;    LENGTH: 19
;    TYPE: RNA
;    ORGANISM: Homo sapiens
US-11-083-784-628845

  Query Match             78.8%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 47;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCT 15
              ||||| |||||||||
Db         18 CTCAGAAACACTCCT 4


RESULT 25
US-11-101-244-628637/c
; Sequence 628637, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 628637
;    LENGTH: 19
;    TYPE: RNA
;    ORGANISM: Homo sapiens
US-11-101-244-628637

  Query Match             78.8%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 47;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCT 15
              ||||| |||||||||
Db         18 CTCAGAAACACTCCT 4


RESULT 26
US-11-101-244-628845/c
; Sequence 628845, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 628845
;    LENGTH: 19
;    TYPE: RNA
;    ORGANISM: Homo sapiens
US-11-101-244-628845

  Query Match             78.8%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 47;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCT 15
              ||||| |||||||||
Db         18 CTCAGAAACACTCCT 4


RESULT 27
US-10-310-914A-273305/c
; Sequence 273305, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 273305
;    LENGTH: 18
;    TYPE: RNA
;    ORGANISM: Human
US-10-310-914A-273305

  Query Match             75.3%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 52;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTA 16
              | ||||||| ||||||
Db         16 CCCAGCAACCCTCCTA 1


RESULT 28
US-10-096-125-14/c
; Sequence 14, Application US/10096125
; Publication No. US20030077608A1
; GENERAL INFORMATION:
;  APPLICANT: Coull, James M.
;  APPLICANT:  Fiandaca, Mark J.
;  APPLICANT:  Kristjanson, Mark D.
```

```
;  APPLICANT:  Hyldig-Nielsen, Jens J.
;  APPLICANT:  Creasey, Theresa S.
;  TITLE OF INVENTION: Methods, Kits And Compositions Pertaining To
;  TITLE OF INVENTION:  Combination Oligomers And Libraries For Their
;  TITLE OF INVENTION:  Preparation
;  FILE REFERENCE: BP0102-US
;  CURRENT APPLICATION NUMBER: US/10/096,125
;  CURRENT FILING DATE:  2002-03-09
;  PRIOR APPLICATION NUMBER: 60/274,547
;  PRIOR FILING DATE: 2001-03-09
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Oligonucleotide Primer
US-10-096-125-14

  Query Match             72.9%;  Score 12.4;  DB 1;  Length 16;
  Best Local Similarity   92.9%;  Pred. No. 51;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TCAGCAACACTCCT 15
              |||||| |||||||
Db         15 TCAGCACCACTCCT 2


RESULT 29
US-10-257-017B-302368/c
; Sequence 302368, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 302368
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0019966
US-10-257-017B-302368

  Query Match             64.7%;  Score 11;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 56;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCTA 16
              |||||||||||
Db         11 CAACACTCCTA 1


RESULT 30
US-10-257-017B-71093/c
; Sequence 71093, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 71093
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0018437
US-10-257-017B-71093

  Query Match             64.7%;  Score 11;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCTA 16
              |||||||||||
Db         13 CAACACTCCTA 3


RESULT 31
US-10-257-017B-71094
; Sequence 71094, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 71094
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0018437
US-10-257-017B-71094

  Query Match             64.7%;  Score 11;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCTA 16
              |||||||||||
Db          1 CAACACTCCTA 11


RESULT 32
US-10-257-017B-136017/c
; Sequence 136017, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 136017
```

```
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0033969
US-10-257-017B-136017

  Query Match             64.7%;  Score 11;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 AACACTCCTAT 17
              ||||||||||
Db         12 AACACTCCTAT 2


RESULT 33
US-10-257-017B-136018
; Sequence 136018, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 136018
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0033969
US-10-257-017B-136018

  Query Match             64.7%;  Score 11;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 AACACTCCTAT 17
              ||||||||||
Db          2 AACACTCCTAT 12


RESULT 34
US-09-848-754A-9312
; Sequence 9312, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Epidermal Growth Factor Receptors
;  FILE REFERENCE: MBHB00-958-I (400/018)
;  CURRENT APPLICATION NUMBER: US/09/848,754A
;  CURRENT FILING DATE:  2001-05-03
;  NUMBER OF SEQ ID NOS: 9645
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9312
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic acid
US-09-848-754A-9312

  Query Match             63.5%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   71.4%;  Pred. No. 75;
  Matches   10;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TCAGCAACACTCCT 15
              :||||||||  ||:
Db          2 UCAGCAACAACCCU 15


RESULT 35
US-10-257-017B-290676/c
; Sequence 290676, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 290676
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014465
US-10-257-017B-290676

  Query Match             61.2%;  Score 10.4;  DB 1;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 66;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCTAT 17
              ||| ||||||||
Db         12 CAAAACTCCTAT 1


RESULT 36
US-10-257-017B-359911/c
; Sequence 359911, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 359911
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0051838
US-10-257-017B-359911

  Query Match             61.2%;  Score 10.4;  DB 1;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 66;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCTAT 17
              ||||| ||||||
Db         12 CAACATTCCTAT 1


RESULT 37
```

```
US-10-257-017B-51767/c
; Sequence 51767, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 51767
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0014432
US-10-257-017B-51767

  Query Match             61.2%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 72;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCTAT 17
              ||||| ||||||
Db         13 CAACATTCCTAT 2


RESULT 38
US-10-257-017B-51768
; Sequence 51768, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 51768
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0014432
US-10-257-017B-51768

  Query Match             61.2%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 72;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCTAT 17
              ||||| ||||||
Db          1 CAACATTCCTAT 12


RESULT 39
US-10-257-017B-159811/c
; Sequence 159811, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 159811
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0040225
US-10-257-017B-159811

  Query Match             61.2%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 72;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CAGCAACACTCC 14
              || |||||||||
Db         12 CAACAACACTCC 1


RESULT 40
US-10-257-017B-159812
; Sequence 159812, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 159812
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0040225
US-10-257-017B-159812

  Query Match             61.2%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 72;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CAGCAACACTCC 14
              || |||||||||
Db          2 CAACAACACTCC 13


RESULT 41
US-10-257-017B-163329/c
; Sequence 163329, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
```

```
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 163329
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0041059
US-10-257-017B-163329

  Query Match             61.2%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 72;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 AGCAACACTCCT 15
              | ||||||||||
Db         12 ACCAACACTCCT 1


RESULT 42
US-10-257-017B-163330
; Sequence 163330, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 163330
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0041059
US-10-257-017B-163330

  Query Match             61.2%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 72;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 AGCAACACTCCT 15
              | ||||||||||
Db          2 ACCAACACTCCT 13


RESULT 43
US-10-257-017B-179987/c
; Sequence 179987, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 179987
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0044568
US-10-257-017B-179987

  Query Match             61.2%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 72;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACT 12
              |||| |||||||
Db         12 CTCATCAACACT 1


RESULT 44
US-10-257-017B-179988
; Sequence 179988, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 179988
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0044568
US-10-257-017B-179988

  Query Match             61.2%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 72;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACT 12
              |||| |||||||
Db          2 CTCATCAACACT 13


RESULT 45
US-10-257-017B-191043/c
; Sequence 191043, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 191043
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0047001
US-10-257-017B-191043

  Query Match             61.2%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 72;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCTAT 17
```

```
                    || |||||||||
Db          12 CACCACTCCTAT 1


RESULT 46
US-10-257-017B-191044
; Sequence 191044, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 191044
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0047001
US-10-257-017B-191044

  Query Match             61.2%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 72;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCTAT 17
              || |||||||||
Db          2 CACCACTCCTAT 13


RESULT 47
US-10-257-017B-222887/c
; Sequence 222887, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 222887
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006573
US-10-257-017B-222887

  Query Match             61.2%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 72;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCTAT 17
              ||| ||||||||
Db         13 CAAAACTCCTAT 2


RESULT 48
US-10-257-017B-222888
; Sequence 222888, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 222888
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006573
US-10-257-017B-222888

  Query Match             61.2%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 72;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCTAT 17
              ||| ||||||||
Db          1 CAAAACTCCTAT 12


RESULT 49
US-10-257-017B-223803/c
; Sequence 223803, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 223803
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0054492
US-10-257-017B-223803

  Query Match             61.2%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 72;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CAACACTCCTAT 17
              ||||| ||||||
Db         13 CAACATTCCTAT 2


RESULT 50
US-10-257-017B-223804
; Sequence 223804, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
```

; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 223804
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0054492
US-10-257-017B-223804

Query Match 61.2%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 72;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CAACACTCCTAT 17
||||| ||||||
Db 1 CAACATTCCTAT 12

Search completed: November 21, 2006, 14:32:49
Job time : 0.001 secs

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: November 21, 2006, 14:35:21 ; Search time 0.001 Seconds
(without alignments)
0.986 Million cell updates/sec

Title: US-10-823-197-7
Perfect score: 17
Sequence: 1 CTCAGCAACACTCCTAT 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 3 seqs, 29 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 3 summaries

Database : rstdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8.4	49.4	12	1	CF543243	ACCESSION:CF543243
c 2	6.4	37.6	9	1	DR026242	ACCESSION:DR026242
c 3	6	35.3	8	1	CL659535	ACCESSION:CL659535

ALIGNMENTS

RESULT 1
CF543243
LOCUS CF543243 12 bp mRNA linear EST 22-SEP-2003
DEFINITION S014680-024-030-N02-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone 024-030-N02 5-PRIME, mRNA sequence.
ACCESSION CF543243
VERSION CF543243.1 GI:34891683
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 12)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 30 row: N column: 02
Seq primer: SP6.
FEATURES Location/Qualifiers
source 1. .12
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:936512"
/db_xref="taxon:161934"
/clone="024-030-N02"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 49.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 CTCAGCAACA 10
              |||| |||||
Db          2 CTCAACAACA 11
```

RESULT 2
DR026242/c
LOCUS DR026242 9 bp mRNA linear EST 26-MAY-2005
DEFINITION Osmo00110 F. cylindrus osmotic stress library Fragilariopsis cylindrus cDNA clone FcylESTa35b12.s1, mRNA sequence.
ACCESSION DR026242
VERSION DR026242.1 GI:66748605
KEYWORDS EST.
SOURCE Fragilariopsis cylindrus
ORGANISM Fragilariopsis cylindrus
Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae; Bacillariophycidae; Bacillariales; Bacillariaceae; Fragilariopsis.
REFERENCE 1 (bases 1 to 9)
AUTHORS Krell,A. and Gloeckner,G.
TITLE Analysis of an osmotic stress induced cDNA library of the psychrophilic diatom Fragilariopsis cylindrus
JOURNAL Unpublished (2004)
COMMENT Contact: Krell, Andreas; Gloeckner, Gernot
Biological Oceanography, Sea ice research; Genome Analysis
Alfred-Wegner-Institute for Polar and Marine Research; Institute for Molecular Biotechnology
Am Handelshafen 12, D-27570 Bremerhaven, Germany; Beutenbergstr. 11, D-07745 Jena, Germany
Tel: ++49 471 48311812; ++49 3641 656440
Fax: ++49 471 48311425; ++49 3641 656255
Email: akrell@awi-bremerhaven.de; gernot@imb-jena.de
PCR PRimers
FORWARD: 5'M13
BACKWARD: 3'M13
Seq primer: 5'GTAAAACGACGGCCAG 3'.
FEATURES Location/Qualifiers
source 1. .9
/organism="Fragilariopsis cylindrus"
/mol_type="mRNA"
/db_xref="taxon:186039"
/clone="FcylESTa35b12.s1"

/clone_lib="F. cylindrus osmotic stress library"
/note="Samples for total RNA isolation were taken continous for 5 days after a salt shock treatment increasing salinity from 34 to 60 PSU. Total RNA extraktion was performed with RNAqueous (Ambion) and mRNA purification with polyA Purist (Ambion). Further steps were carried out as described in the Cloneminer Kit. cDNA size fractionation was carried out with CHROMA Spin-400 columns and additionally on a gel."

Query Match 37.6%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          7 AACACTCC 14
              || |||||
Db          9 AAAACTCC 2
```

RESULT 3
CL659535/c
LOCUS CL659535 8 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0134b_G05 - PRI0134b.B21 (8) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION CL659535
VERSION CL659535.1 GI:50143739
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 8)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppaDB: an AcedB database for the nematode satellite organism Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
PUBMED 14681447
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES Location/Qualifiers
source 1. .8
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pEpifos-5 Fosmid vector"

Query Match 35.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 TCAGCA 7
              ||||||
Db          7 TCAGCA 2
```

Search completed: November 21, 2006, 14:35:21
Job time : 0.001 secs

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: November 21, 2006, 14:30:59 ; Search time 0.001 Seconds
(without alignments)
24.276 Million cell updates/sec

Title: US-10-823-197-7
Perfect score: 17
Sequence: 1 CTCAGCAACACTCCTAT 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 64 seqs, 714 residues

Total number of hits satisfying chosen parameters: 128

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 64 summaries

Database : rnidb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	17	100.0	17	1	US-08-628-282-1	Sequence 1, Appli
	2	17	100.0	17	1	US-08-587-911-1	Sequence 1, Appli
	3	17	100.0	17	1	US-08-813-456-1	Sequence 1, Appli
	4	17	100.0	17	1	US-09-345-217-22	Sequence 22, Appl
	5	17	100.0	17	1	US-09-431-352-1	Sequence 1, Appli
	6	17	100.0	17	1	US-09-845-129-22	Sequence 22, Appl
	7	17	100.0	17	1	US-09-037-472-5	Sequence 5, Appli
	8	17	100.0	17	1	US-09-578-534-7	Sequence 7, Appli
	9	17	100.0	17	1	US-09-632-657-9	Sequence 9, Appli
	10	17	100.0	17	1	US-09-693-555A-15	Sequence 15, Appl
	11	17	100.0	17	1	US-09-584-950-13	Sequence 13, Appl
c	12	10.8	63.5	15	1	US-08-373-124A-95	Sequence 95, Appl
c	13	10.8	63.5	15	1	US-08-435-628-95	Sequence 95, Appl
c	14	9	52.9	11	1	US-09-249-155A-146	Sequence 146, App
	15	9	52.9	12	1	US-09-491-356C-10	Sequence 10, Appl
	16	8.4	49.4	12	1	US-09-281-418-146	Sequence 146, App
c	17	8.4	49.4	12	1	US-09-210-952-39	Sequence 39, Appl
c	18	8	47.1	9	1	US-09-990-186-2463	Sequence 2463, Ap
c	19	8	47.1	9	1	US-09-990-186-2464	Sequence 2464, Ap
	20	8	47.1	10	1	US-09-508-753B-65	Sequence 65, Appl
c	21	8	47.1	10	1	US-09-508-753B-78	Sequence 78, Appl
	22	8	47.1	11	1	US-08-891-789B-11	Sequence 11, Appl
c	23	7.4	43.5	9	1	US-09-990-186-59	Sequence 59, Appl
c	24	7.4	43.5	9	1	US-09-990-186-60	Sequence 60, Appl
c	25	7.4	43.5	9	1	US-09-990-186-61	Sequence 61, Appl
c	26	7.4	43.5	9	1	US-09-990-186-119	Sequence 119, App
c	27	7.4	43.5	9	1	US-09-990-186-2353	Sequence 2353, Ap
c	28	7.4	43.5	9	1	US-09-990-186-2356	Sequence 2356, Ap
c	29	7.4	43.5	9	1	US-09-990-186-2357	Sequence 2357, Ap
c	30	7.4	43.5	9	1	US-09-990-186-2431	Sequence 2431, Ap
c	31	7.4	43.5	9	1	US-09-990-186-2462	Sequence 2462, Ap
c	32	7.4	43.5	10	1	US-08-388-353-534	Sequence 534, App
c	33	7.4	43.5	10	1	US-08-388-353-535	Sequence 535, App
c	34	7.4	43.5	10	1	US-08-488-551B-534	Sequence 534, App
c	35	7.4	43.5	10	1	US-08-488-551B-535	Sequence 535, App
c	36	7.4	43.5	10	1	US-08-088-661F-37	Sequence 37, Appl
c	37	7.4	43.5	10	1	US-09-173-936B-1	Sequence 1, Appli
c	38	7.4	43.5	10	1	US-08-108-591B-35	Sequence 35, Appl
c	39	7.4	43.5	10	1	US-09-632-538C-7	Sequence 7, Appli
	40	7.4	43.5	10	1	US-08-479-660-16	Sequence 16, Appl
c	41	7.4	43.5	10	1	US-09-627-536-7	Sequence 7, Appli
c	42	7.4	43.5	10	1	US-08-894-454-120	Sequence 120, App
	43	7.4	43.5	10	1	US-09-525-906-10	Sequence 10, Appl
c	44	7.4	43.5	10	1	US-08-468-719A-35	Sequence 35, Appl
c	45	7.4	43.5	10	1	US-08-462-977B-35	Sequence 35, Appl
c	46	7.4	43.5	10	1	US-09-641-540-7	Sequence 7, Appli
c	47	7.4	43.5	10	1	US-09-748-710-24	Sequence 24, Appl
	48	7.4	43.5	10	1	PCT-US96-09383-16	Sequence 16, Appl
c	49	7	41.2	8	1	US-08-859-954-7	Sequence 7, Appli
	50	7	41.2	8	1	US-08-859-954-314	Sequence 314, App
c	51	7	41.2	8	1	US-08-859-954-335	Sequence 335, App
c	52	7	41.2	8	1	US-08-859-954-452	Sequence 452, App
c	53	7	41.2	9	1	US-09-990-186-453	Sequence 453, App
c	54	7	41.2	9	1	US-09-990-186-454	Sequence 454, App
c	55	7	41.2	10	1	US-09-593-323-55	Sequence 55, Appl
c	56	7	41.2	10	1	US-09-594-108-55	Sequence 55, Appl
c	57	7	41.2	10	1	US-09-344-300-55	Sequence 55, Appl
c	58	7	41.2	10	1	US-09-101-272G-91	Sequence 91, Appl
c	59	7	41.2	10	1	US-09-508-753B-61	Sequence 61, Appl
	60	7	41.2	10	1	US-09-508-753B-159	Sequence 159, App
c	61	7	41.2	10	1	US-09-825-770-1	Sequence 1, Appli
c	62	7	41.2	10	1	US-10-677-496-1	Sequence 1, Appli
	63	7	41.2	10	1	US-09-263-790-23	Sequence 23, Appl
	64	7	41.2	10	1	US-09-721-777-3	Sequence 3, Appli

ALIGNMENTS

```
RESULT 1
US-08-628-282-1
; Sequence 1, Application US/08628282
; Patent No. 5698399
;  GENERAL INFORMATION:
;    APPLICANT:  Duff, Gordon W.
;    APPLICANT:  Russell, Graham
;    APPLICANT:  Eastell, Richard
;    TITLE OF INVENTION:  DETECTING GENETIC PREDISPOSITION FOR
;    TITLE OF INVENTION:  OSTEOPOROSIS
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Aquilino & Welsh
;      STREET:  2121 Crystal Drive, Suite 503
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  US
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/628,282
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Welsh, John L.
;      REGISTRATION NUMBER:  33,621
;      REFERENCE/DOCKET NUMBER:  MSS-005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 920-1122
;      TELEFAX:  (703) 920-3399
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
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;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-628-282-1

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 0.083;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 2
US-08-587-911-1
; Sequence 1, Application US/08587911
; Patent No. 5942390
;  GENERAL INFORMATION:
;    APPLICANT:  Cominelli M.D., Fabio
;    APPLICANT:  Pizarro Ph.D., Theresa
;    APPLICANT:  Rotter M.D., Jerome I.
;    APPLICANT:  Yang M.D., Huiying
;    TITLE OF INVENTION:  METHODS OF SCREENING FOR ULCERATIVE
;    TITLE OF INVENTION:  COLITIS BY DETECTING AN INTERLEUKIN-1 RECEPTOR ANTAGONIST
;    TITLE OF INVENTION:  POLYMORPHISM
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pretty, Schroeder, Brueggemann & Clark
;      STREET:  444 South Flower Street, Suite 2000
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/587,911
;      FILING DATE:  January 12, 1996
;      CLASSIFICATION:  538
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Whiteford Esq., Wendy A
;      REGISTRATION NUMBER:  36,964
;      REFERENCE/DOCKET NUMBER:  P07 34246
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  213-622-7700
;      TELEFAX:  213-489-4210
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
US-08-587-911-1

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 0.083;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 3
US-08-813-456-1
; Sequence 1, Application US/08813456
; Patent No. 6210877
;  GENERAL INFORMATION:
;    APPLICANT:  Francis, Sheila
;    APPLICANT:  Crossman, David
;    APPLICANT:  Duff, Gordon
;    TITLE OF INVENTION:  Prediction of Coronary Artery
;    TITLE OF INVENTION:  Disease
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jenkens & Gilchrist
;      STREET:  1100 Louisiana, Suite 1800
;      CITY:  Houston
;      STATE:  TX
;      COUNTRY:  USA
;      ZIP:  77002
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/813,456
;      FILING DATE:  10-MAR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Turley, Charles P
;      REGISTRATION NUMBER:  35,723
;      REFERENCE/DOCKET NUMBER:  33174-00003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (713)9513310
;      TELEFAX:  (713)9513314
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-813-456-1

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 0.083;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 4
US-09-345-217-22
; Sequence 22, Application US/09345217
; Patent No. 6268142
; GENERAL INFORMATION:
;  APPLICANT: DUFF, GORDON W.
;  APPLICANT: COX, ANGELA
;  APPLICANT: CAMP, NICOLA J.
;  APPLICANT: DIGIOVINE, FRANCESCO S.
;  TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR DISEASES ASSOCIATED
;  TITLE OF INVENTION: WITH AN IL-1 INFLAMMATORY HAPLOTYPE
;  FILE REFERENCE: MSA-010.02
;  CURRENT APPLICATION NUMBER: US/09/345,217
;  CURRENT FILING DATE: 1999-06-30
;  EARLIER APPLICATION NUMBER: PCT/GB98/01481
;  EARLIER FILING DATE: 1998-05-21
;  EARLIER APPLICATION NUMBER: 9711040.7
;  EARLIER FILING DATE: 1997-05-29
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
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;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-345-217-22

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 0.083;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 5
US-09-431-352-1
; Sequence 1, Application US/09431352
; Patent No. 6524795
; GENERAL INFORMATION:
;  APPLICANT:  Francis, Sheila E.
;  APPLICANT:  Crossman, David C.
;  APPLICANT:  Duff, Gordon W.
;  APPLICANT:  Kornman, Kenneth S.
;  APPLICANT:  Stephenson, Katherine
;  TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS FOR CARDIOVASCULAR
;  TITLE OF INVENTION:  DISORDERS
;  FILE REFERENCE:  MSA-006.03
;  CURRENT APPLICATION NUMBER: US/09/431,352
;  CURRENT FILING DATE:  1999-11-01
;  PRIOR APPLICATION NUMBER:  09/320,395
;  PRIOR FILING DATE:  1999-05-26
;  NUMBER OF SEQ ID NOS:  18
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-431-352-1

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 0.083;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 6
US-09-845-129-22
; Sequence 22, Application US/09845129
; Patent No. 6706478
; GENERAL INFORMATION:
;  APPLICANT: DUFF, GORDON W.
;  APPLICANT:  COX, ANGELA
;  APPLICANT:  CAMP, NICOLA J.
;  APPLICANT:  DIGIOVINE, FRANCESCO S.
;  TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR DISEASES ASSOCIATED
;  TITLE OF INVENTION:  WITH AN IL-1 INFLAMMATORY HAPLOTYPE
;  FILE REFERENCE: MSA-010.02
;  CURRENT APPLICATION NUMBER: US/09/845,129
;  CURRENT FILING DATE:  2001-04-27
;  PRIOR APPLICATION NUMBER: 09/345,217
;  PRIOR FILING DATE: 1999-06-30
;  PRIOR APPLICATION NUMBER: PCT/GB98/01481
;  PRIOR FILING DATE: 1998-05-21
;  PRIOR APPLICATION NUMBER: 9711040.7
;  PRIOR FILING DATE: 1997-05-29
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-845-129-22

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 0.083;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 7
US-09-037-472-5
; Sequence 5, Application US/09037472
; Patent No. 6713253
;  GENERAL INFORMATION:
;    APPLICANT:  Duff, Gordon W.
;    APPLICANT:  Richardson, Robert R.S.
;    APPLICANT:  Rennie, Ian G.
;    TITLE OF INVENTION:  DETECTING GENETIC PREDISPOSITION TO
;    TITLE OF INVENTION:  SIGHT-THREATENING DIABETIC RETINOPATHY
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2170
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/037,472
;      FILING DATE:  10-MAR-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB97/02790
;      FILING DATE:  09-OCT-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold, Beth E.
;      REGISTRATION NUMBER:  35,430
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 832-1000
;      TELEFAX:  (617) 832-7000
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "primer"
US-09-037-472-5

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 0.083;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17
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```
RESULT 8
US-09-578-534-7
; Sequence 7, Application US/09578534
; Patent No. 6720141
; GENERAL INFORMATION:
;  APPLICANT: CROSSMAN, DAVID C.
;  APPLICANT:  DUFF, GORDON W.
;  APPLICANT:  FRANCIS, SHEILA E.
;  APPLICANT:  KORNMAN, KENNETH S.
;  APPLICANT:  STEPHENSON, KATHERINE
;  TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR RESTENOSIS
;  FILE REFERENCE: MSA-017.02
;  CURRENT APPLICATION NUMBER: US/09/578,534
;  CURRENT FILING DATE:  2000-05-24
;  PRIOR APPLICATION NUMBER: 09/431,352
;  PRIOR FILING DATE: 1999-11-01
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-578-534-7

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 0.083;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 9
US-09-632-657-9
; Sequence 9, Application US/09632657
; Patent No. 6730476
; GENERAL INFORMATION:
;  APPLICANT: DUFF, GORDON
;  APPLICANT:  KORNMAN, KENNETH
;  APPLICANT:  VAN DIJK, SIMON
;  TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR EARLY-ONSET MENOPAUSE
;  FILE REFERENCE: MSA-012.01
;  CURRENT APPLICATION NUMBER: US/09/632,657
;  CURRENT FILING DATE:  2000-08-04
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide
US-09-632-657-9

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 0.083;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 10
US-09-693-555A-15
; Sequence 15, Application US/09693555A
; Patent No. 6733967
; GENERAL INFORMATION:
;  APPLICANT: KORNMAN, KENNETH
;  APPLICANT:  DUFF, GORDON
;  APPLICANT:  OFFENBACHER, STEVEN
;  TITLE OF INVENTION: FETAL TESTING FOR PREDICTION OF LOW BIRTH WEIGHT
;  FILE REFERENCE: MSA-009.01
;  CURRENT APPLICATION NUMBER: US/09/693,555A
;  CURRENT FILING DATE:  2000-10-20
;  PRIOR APPLICATION NUMBER: PCT/US99/08794
;  PRIOR FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: 60/082,487
;  PRIOR FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-693-555A-15

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 0.083;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 11
US-09-584-950-13
; Sequence 13, Application US/09584950
; Patent No. 6746839
; GENERAL INFORMATION:
;  APPLICANT: DUFF, GORDON W.
;  APPLICANT:  DI GIOVINE, FRANCESCO S.
;  APPLICANT:  BARNES, PETER J.
;  APPLICANT:  LIM, SAMSON
;  TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR AN OBSTRUCTIVE AIRWAY
;  TITLE OF INVENTION:  DISEASE
;  FILE REFERENCE: MSA-005.02
;  CURRENT APPLICATION NUMBER: US/09/584,950
;  CURRENT FILING DATE:  2000-06-01
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-584-950-13

  Query Match             100.0%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 0.083;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCCTAT 17
              |||||||||||||||||
Db          1 CTCAGCAACACTCCTAT 17


RESULT 12
US-08-373-124A-95/c
; Sequence 95, Application US/08373124A
; Patent No. 5646042
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
```

```
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/373,124A
;      FILING DATE:  January 13, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  95:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-373-124A-95

  Query Match             63.5%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 2.3;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCC 14
              ||||||||||  | |
Db         14 CTCAGCAACAATTC 1


RESULT 13
US-08-435-628-95/c
; Sequence 95, Application US/08435628
; Patent No. 5817796
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Jarvis, Thale
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TREATMENT OF RESTENOSIS AND
;    TITLE OF INVENTION:  CANCER USING RIBOZYMES
;    NUMBER OF SEQUENCES:  2627
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,628
;      FILING DATE:  05-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/373,124
;      FILING DATE:  January 13, 1995
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  08/192,943
;      FILING DATE:  February 7, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;      APPLICATION NUMBER:  07/936,422
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  209/035
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  95:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-435-628-95

  Query Match             63.5%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 2.3;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAACACTCC 14
              ||||||||||  | |
Db         14 CTCAGCAACAATTC 1


RESULT 14
US-09-249-155A-146/c
; Sequence 146, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
;  APPLICANT:  Heber-Katz, Ellen
;  TITLE OF INVENTION:  Compositions and Methods for Wound
;  TITLE OF INVENTION:  Healing
;  FILE REFERENCE:  00486.78503
;  CURRENT APPLICATION NUMBER: US/09/249,155A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER:  US 60/074,737
;  PRIOR FILING DATE:  1998-02-13
;  PRIOR APPLICATION NUMBER:  US 60/097,937
;  PRIOR FILING DATE:  1998-08-26
;  PRIOR APPLICATION NUMBER:  US 60/102,051
;  PRIOR FILING DATE:  1998-09-28
;  NUMBER OF SEQ ID NOS:  346
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 146
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-249-155A-146
```

Query Match 52.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCAGCAAC 9
|||||||||
Db 9 CTCAGCAAC 1

RESULT 15
US-09-491-356C-10
; Sequence 10, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Ginns, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6USI1
; CURRENT APPLICATION NUMBER: US/09/491,356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-491-356C-10

Query Match 52.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CAGCAACAC 11
|||||||||
Db 1 CAGCAACAC 9

RESULT 16
US-09-281-418-146
; Sequence 146, Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA F
; TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing Mi
; TITLE OF INVENTION: nisms and Method of Assaying Contaminant
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281,418
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: JP/1998/87651
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 146
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-281-418-146

Query Match 49.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 9.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTCAGCAACA 10
|| |||||||
Db 2 CTGAGCAACA 11

RESULT 17
US-09-210-952-39/c
; Sequence 39, Application US/09210952A
; Patent No. 6624288
; GENERAL INFORMATION:
; APPLICANT: Fainzilber, Michael M.
; APPLICANT: Kits, Karel S.
; APPLICANT: Burlingame, Alma L.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Walker, Craig
; APPLICANT: Watkins, Maren
; APPLICANT: Shetty, Reshma
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Imperial, Julita
; APPLICANT: Colledge, Clark
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Vrije Universiteit
; APPLICANT: Regents of the University of California
; TITLE OF INVENTION: Gamma-Conopeptides
; FILE REFERENCE: Gamma-Conpeptides
; CURRENT APPLICATION NUMBER: US/09/210,952A
; CURRENT FILING DATE: 1998-12-15
; EARLIER APPLICATION NUMBER: US 60/069,706
; EARLIER FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:degenerate
; OTHER INFORMATION: probe for consensus gamma-conopeptide sequence.
US-09-210-952-39

Query Match 49.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 9.6;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AGCAACACTC 13
|:||:||:|:
Db 10 ARCARCAYTS 1

RESULT 18
US-09-990-186-2463/c
; Sequence 2463, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2463
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-2463

Query Match 47.1%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          7 AACACTCC 14
              ||||||||
Db          8 AACACTCC 1


RESULT 19
US-09-990-186-2464/c
; Sequence 2464, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2464
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2464

  Query Match             47.1%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 AACACTCC 14
              ||||||||
Db          8 AACACTCC 1


RESULT 20
US-09-508-753B-65
; Sequence 65, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 65
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-65

  Query Match             47.1%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TCAGCAAC 9
              ||||||||
Db          1 TCAGCAAC 8


RESULT 21
US-09-508-753B-78/c
; Sequence 78, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 78
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-78

  Query Match             47.1%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAA 8
              ||||||||
Db          8 CTCAGCAA 1


RESULT 22
US-08-891-789B-11
; Sequence 11, Application US/08891789B
; Patent No. 6103466
;  GENERAL INFORMATION:
;    APPLICANT:  Grobet, Luc; Georges, Michel
;    TITLE OF INVENTION:  Double-Muscling in Mammals
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Blake, Cassels & Graydon
;      STREET:  Box 25, Commerce Court West
;      CITY:  Toronto
;      STATE:  Ontario
;      ZIP:  M5L 1A9
;      COUNTRY:  Canada
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3 1/2 inch, 1.4 Mb storage
;      COMPUTER:  COMPAQ, IBM PC compatible
;      OPERATING SYSTEM:  MS-DOS 5.1
;      SOFTWARE:  WORD PERFECT
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/891,789B
;      FILING DATE:  July 14, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunt, John C.
;      REGISTRATION NUMBER:  36,424
;      REFERENCE/DOCKET NUMBER:  52836/00004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 863-4344
;      TELEFAX:  (416) 863-2653
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-891-789B-11

  Query Match             47.1%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 13;
```

```
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 AACACTCC 14
              ||||||||
Db          4 AACACTCC 11


RESULT 23
US-09-990-186-59/c
; Sequence 59, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-59

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAAC 9
              ||||||| |
Db          9 CTCAGCATC 1


RESULT 24
US-09-990-186-60/c
; Sequence 60, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-60

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAAC 9
              ||||||| |
Db          9 CTCAGCATC 1


RESULT 25
US-09-990-186-61/c
; Sequence 61, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-61

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAAC 9
              ||||||| |
Db          9 CTCAGCATC 1


RESULT 26
US-09-990-186-119/c
; Sequence 119, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-119

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAAC 9
              ||||||| |
Db          9 CTCAGCATC 1


RESULT 27
US-09-990-186-2353/c
; Sequence 2353, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2353
;   LENGTH: 9
```

```
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2353

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred..No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ACACTCCTA 16
              | |||||||
Db          9 AAACTCCTA 1


RESULT 28
US-09-990-186-2356/c
; Sequence 2356, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2356
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2356

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ACACTCCTA 16
              | |||||||
Db          9 AAACTCCTA 1


RESULT 29
US-09-990-186-2357/c
; Sequence 2357, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2357
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2357

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ACACTCCTA 16
              | |||||||
Db          9 AAACTCCTA 1


RESULT 30
US-09-990-186-2431/c
; Sequence 2431, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2431
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2431

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ACACTCCTA 16
              ||||||| |
Db          9 ACACTCCCA 1


RESULT 31
US-09-990-186-2462/c
; Sequence 2462, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2462
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2462

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ACACTCCTA 16
              ||||||| |
Db          9 ACACTCCCA 1


RESULT 32
US-08-388-353-534/c
; Sequence 534, Application US/08388353
; Patent No. 6010895
;  GENERAL INFORMATION:
;    APPLICANT:  Deacon, Nicholas J.
```

```
;    APPLICANT:  Learmont, Jennifer C.
;    APPLICANT:  McPhee, Dale A.
;    APPLICANT:  Crowe, Suzanne
;    APPLICANT:  Cooper, David
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  800
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/388,353
;      FILING DATE:  14-FEB-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9606
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  534:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-388-353-534

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 AACACTCCT 15
              |||||| ||
Db         10 AACACTTCT 2


RESULT 33
US-08-388-353-535/c
; Sequence 535, Application US/08388353
; Patent No. 6010895
;  GENERAL INFORMATION:
;    APPLICANT:  Deacon, Nicholas J.
;    APPLICANT:  Learmont, Jennifer C.
;    APPLICANT:  McPhee, Dale A.
;    APPLICANT:  Crowe, Suzanne
;    APPLICANT:  Cooper, David
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  800
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/388,353
;      FILING DATE:  14-FEB-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  9606
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  535:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-388-353-535

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 AACACTCCT 15
              |||||| ||
Db          9 AACACTTCT 1


RESULT 34
US-08-488-551B-534/c
; Sequence 534, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  534:
;    SEQUENCE CHARACTERISTICS:
```

```
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-534

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 AACACTCCT 15
              |||||| ||
Db         10 AACACTTCT 2


RESULT 35
US-08-488-551B-535/c
; Sequence 535, Application US/08488551B
; Patent No. 6015661
;  GENERAL INFORMATION:
;    APPLICANT:  Nicholas J. Deacon
;    APPLICANT:  Dale A. McPhee
;    APPLICANT:  David Cooper
;    TITLE OF INVENTION:  NON-PATHOGENIC STRAINS OF HIV-1
;    NUMBER OF SEQUENCES:  841
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 GARDEN CITY PLAZA
;      CITY:  GARDEN CITY
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  11530-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,551B
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PM3864 (AU)
;      FILING DATE:  14-FEB-1994
;      APPLICATION NUMBER:  PM4002 (AU)
;      FILING DATE:  21-FEB-1994
;      APPLICATION NUMBER:  PN0284 (AU)
;      FILING DATE:  23-DEC-1994
;      APPLICATION NUMBER:  US 08/388,353
;      FILING DATE:  14-FEB-1995
;      APPLICATION NUMBER:  PN3021/95
;      FILING DATE:  17-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FRANK S. DIGIGLIO
;      REFERENCE/DOCKET NUMBER:  9606Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;  INFORMATION FOR SEQ ID NO:  535:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-488-551B-535

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 AACACTCCT 15
              |||||| ||
Db          9 AACACTTCT 1


RESULT 36
US-08-088-661F-37/c
; Sequence 37, Application US/08088661F
; Patent No. 6228982
; GENERAL INFORMATION:
;  APPLICANT:  No. 6228982den, Benget
;  APPLICANT:  Wittung, Pernilla
;  APPLICANT:  Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter E.
;  APPLICANT:  Berg, Rolf
;  TITLE OF INVENTION:  Double-Stranded Peptide Nucleic Acids
;  FILE REFERENCE:  ISIS1108
;  CURRENT APPLICATION NUMBER: US/08/088,661F
;  CURRENT FILING DATE:  1993-07-02
;  PRIOR APPLICATION NUMBER:  08/054,363
;  PRIOR FILING DATE:  1993-04-26
;  PRIOR APPLICATION NUMBER:  PCT/EP92/01219
;  PRIOR FILING DATE:  1992-05-19
;  NUMBER OF SEQ ID NOS:  42
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 37
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: No. 6228982el Sequence
US-08-088-661F-37

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 CACTCCTAT 17
              |||| ||||
Db         10 CACTACTAT 2


RESULT 37
US-09-173-936B-1/c
; Sequence 1, Application US/09173936B
; Patent No. 6238865
;   GENERAL INFORMATION:
;        APPLICANT: Zhen, Huang; Szostak, Jack W.
;        TITLE OF INVENTION: A Simple and Efficient Method to Label and Modify 3'-
;                            Terminal
;                            of RNA Using DNA Polymerase and a Synthetic Template with D
;                            Nucleotides
;        NUMBER OF SEQUENCES: 21
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Cohen,Pontani,Lieberman & Pavane
;             STREET: 551 Fifth Avenue
;             CITY: New York
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10176
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.50 inch Diskette
;             COMPUTER: IBM-MS
;             OPERATING SYSTEM: Window 95
;             SOFTWARE: Microsoft Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/173,936B
;             FILING DATE: 16-Oct-1998
;             CLASSIFICATION: 435
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/063,757
;             FILING DATE: 17-OCT-1997
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
```

```
;             LENGTH: 10 bases
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-173-936B-1

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CAGCAACAC 11
              ||||||| |
Db          9 CAGCAACCC 1


RESULT 38
US-08-108-591B-35/c
; Sequence 35, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: Peptide Nucleic Acids
;  FILE REFERENCE: ISIS0540
;  CURRENT APPLICATION NUMBER: US/08/108,591B
;  CURRENT FILING DATE:  2001-08-13
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-35

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 CACTCCTAT 17
              |||| ||||
Db         10 CACTACTAT 2


RESULT 39
US-09-632-538C-7/c
; Sequence 7, Application US/09632538C
; Patent No. 6440674
; GENERAL INFORMATION:
;  APPLICANT: Misra, Santosh et al.
;  TITLE OF INVENTION: PLANT PROMOTER DERIVED FROM LUMINAL BINDING PROTEIN GENE AND METH
;  TITLE OF INVENTION:  ITS USE
;  FILE REFERENCE: 54359
;  CURRENT APPLICATION NUMBER: US/09/632,538C
;  CURRENT FILING DATE:  2000-08-04
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: PROMOTER
;   OTHER INFORMATION: ELEMENT
US-09-632-538C-7

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAAC 9
              |||| ||||
Db          9 CTCAACAAC 1


RESULT 40
US-08-479-660-16
; Sequence 16, Application US/08479660
; Patent No. 6475806
;  GENERAL INFORMATION:
;    APPLICANT:  Benjamin, Howard
;    APPLICANT:  Signer, Ethan
;    APPLICANT:  Gefter, Malcolm
;    TITLE OF INVENTION:  ANCHOR LIBRARIES AND IDENTIFICATION
;    TITLE OF INVENTION:  OF PEPTIDE BINDING SEQUENCES
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/479,660
;      FILING DATE:  __________, 1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Greer, Helen
;      REGISTRATION NUMBER:  36,816
;      REFERENCE/DOCKET NUMBER:  P0567/7000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 720-3500
;      TELEFAX:  (617) 720-2441
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-479-660-16

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CAGCAACAC 11
              ||||| |||
Db          1 CAGCACCAC 9


RESULT 41
US-09-627-536-7/c
; Sequence 7, Application US/09627536
; Patent No. 6541222
; GENERAL INFORMATION:
;  APPLICANT:  Misra, Santosh et al.,
;  TITLE OF INVENTION:  PLANT GENE PROMOTER ISOLATED FROM DOUGLAS-FIR 2S SEED STORAGE PR
;  FILE REFERENCE:  54094
;  CURRENT APPLICATION NUMBER: US/09/627,536
;  CURRENT FILING DATE:  2000-07-28
;  NUMBER OF SEQ ID NOS:  18
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 10
;   TYPE: DNA
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```
;   ORGANISM: Pseudotsuga menziesii
US-09-627-536-7

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAAC 9
              |||| ||||
Db          9 CTCAACAAC 1


RESULT 42
US-08-894-454-120/c
; Sequence 120, Application US/08894454
; Patent No. 6544784
;  GENERAL INFORMATION:
;    APPLICANT:  VAN DEN VEN, W.J.M.
;    APPLICANT:  SCHOENMAKERS, H.F.P.M.
;    TITLE OF INVENTION:  MULTIPLE-TUMOR ABERRENT GROWTH
;    TITLE OF INVENTION:  GENES
;    NUMBER OF SEQUENCES:  164
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  The Webb Law Firm
;      STREET:  700 Koppers Building, 436 Seventh Avenue
;      CITY:  Pittsburgh
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  15219-1818
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/894,454
;      FILING DATE:  15-AUG-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP/00716
;      FILING DATE:  19-FEB-1996
;      APPLICATION NUMBER:  95200390.3
;      FILING DATE:  17-FEB-1995
;      APPLICATION NUMBER:  95201951.1
;      FILING DATE:  14-JUL-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Johnson, Barbara E
;      REGISTRATION NUMBER:  31,198
;      REFERENCE/DOCKET NUMBER:  702-971100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  412-471-8815
;      TELEFAX:  412-471-4094
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  120:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-894-454-120

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 AACACTCCT 15
              || ||||||
Db         10 AAAACTCCT 2


RESULT 43
US-09-525-906-10
; Sequence 10, Application US/09525906
; Patent No. 6605433
; GENERAL INFORMATION:
;  APPLICANT:  Jen, Jen
;  APPLICANT:  Sidransky, David
;  APPLICANT:  Kinzler, Kenneth
;  APPLICANT:  Vogelstein, Bert
;  APPLICANT:  Fliss, Makiko
;  APPLICANT:  Polyak, Kornelia
;  TITLE OF INVENTION:  Mitochondrial Dosimeter
;  FILE REFERENCE:  1107.85815
;  CURRENT APPLICATION NUMBER: US/09/525,906
;  CURRENT FILING DATE:  2000-03-15
;  PRIOR APPLICATION NUMBER:  09/377,856
;  PRIOR FILING DATE:  1999-08-20
;  PRIOR APPLICATION NUMBER:  60/097,307
;  PRIOR FILING DATE:  1998-08-20
;  NUMBER OF SEQ ID NOS:  11
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 10
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-525-906-10

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ACACTCCTA 16
              ||||| |||
Db          2 ACACTACTA 10


RESULT 44
US-08-468-719A-35/c
; Sequence 35, Application US/08468719A
; Patent No. 6710163
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter E.
;  APPLICANT:  Berg, Rolf H.
;  TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS SYNTHONS
;  FILE REFERENCE: ISPS-1999
;  CURRENT APPLICATION NUMBER: US/08/468,719A
;  CURRENT FILING DATE:  1995-06-06
;  PRIOR APPLICATION NUMBER: US 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide Primer
US-08-468-719A-35

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 CACTCCTAT 17
              |||| ||||
Db         10 CACTACTAT 2


RESULT 45
US-08-462-977B-35/c
; Sequence 35, Application US/08462977B
; Patent No. 6713602
; GENERAL INFORMATION:
;  APPLICANT: Buchardt, Ole
```

```
;  APPLICANT:  Egholm, Michael
;  APPLICANT:  Nielsen, Peter Eigil
;  APPLICANT:  Berg, Rolf Henrik
;  TITLE OF INVENTION: Peptide Nucleic Acids
;  FILE REFERENCE: ISIS-1993
;  CURRENT APPLICATION NUMBER: US/08/462,977B
;  CURRENT FILING DATE:  1995-06-05
;  PRIOR APPLICATION NUMBER: 08/108,591
;  PRIOR FILING DATE: 1993-11-22
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: No. 6713602el Sequence
US-08-462-977B-35

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 CACTCCTAT 17
              |||| ||||
Db         10 CACTACTAT 2


RESULT 46
US-09-641-540-7/c
; Sequence 7, Application US/09641540
; Patent No. 6759529
; GENERAL INFORMATION:
;  APPLICANT:  Misra, Santosh
;  TITLE OF INVENTION:  PLANT-GENE PROMOTER AND METHODS OF USING THE SAME
;  FILE REFERENCE:  54358
;  CURRENT APPLICATION NUMBER: US/09/641,540
;  CURRENT FILING DATE:  2000-08-18
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: PROMOTER
;   OTHER INFORMATION: ELEMENT
US-09-641-540-7

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTCAGCAAC 9
              |||| ||||
Db          9 CTCAACAAC 1


RESULT 47
US-09-748-710-24/c
; Sequence 24, Application US/09748710
; Patent No. 6916610
; GENERAL INFORMATION:
;  APPLICANT: WANG, SAN MING
;  APPLICANT:  CHEN, JIANJUN
;  APPLICANT:  ROWLEY, JANET D.
;  TITLE OF INVENTION: METHOD FOR GENERATION OF LONGER cDNA FRAGMENTS
;  TITLE OF INVENTION:  FROM SAGE TAGS FOR GENE IDENTIFICATION
;  FILE REFERENCE: ARCD:343US
;  CURRENT APPLICATION NUMBER: US/09/748,710
;  CURRENT FILING DATE:  2000-12-22
;  PRIOR APPLICATION NUMBER: 60/174,391
;  PRIOR FILING DATE: 2000-01-03
;  PRIOR APPLICATION NUMBER: 60/173,617
;  PRIOR FILING DATE: 1999-12-29
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Primer
US-09-748-710-24

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TCAGCAACA 10
              ||| |||||
Db         10 TCACCAACA 2


RESULT 48
PCT-US96-09383-16
; Sequence 16, Application PC/TUS9609383
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  ANCHOR LIBRARIES AND IDENTIFICATION                O
;    TITLE OF INVENTION:  PEPTIDE BINDING SEQUENCES
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/09383
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/479,660
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Greer, Helen
;      REGISTRATION NUMBER:  36,816
;      REFERENCE/DOCKET NUMBER:  P0567/7000WO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 720-3500
;      TELEFAX:  (617) 720-2441
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US96-09383-16

  Query Match             43.5%;  Score 7.4;  DB 1;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 CAGCAACAC 11
              ||||| |||
Db          1 CAGCACCAC 9
```

```
RESULT 49
US-08-859-954-7/c
; Sequence 7, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-7

  Query Match          41.2%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 1.4e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TCAGCAA 8
              |||||||
Db          7 TCAGCAA 1


RESULT 50
US-08-859-954-314
; Sequence 314, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  314:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-314

  Query Match          41.2%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 1.4e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCA 7
              |||||||
Db          1 CTCAGCA 7


RESULT 51
US-08-859-954-335/c
; Sequence 335, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
```

```
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  335:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-335

  Query Match             41.2%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 ACACTCC 14
              |||||||
Db          8 ACACTCC 2


RESULT 52
US-08-859-954-452/c
; Sequence 452, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  452:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-452

  Query Match             41.2%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 CACTCCT 15
              |||||||
Db          7 CACTCCT 1


RESULT 53
US-09-990-186-453/c
; Sequence 453, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 453
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-453

  Query Match             41.2%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CAGCAAC 9
              |||||||
Db          7 CAGCAAC 1


RESULT 54
US-09-990-186-454/c
; Sequence 454, Application US/09990186
; Patent No. 7030215
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 454
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-454

  Query Match             41.2%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CAGCAAC 9
              |||||||
```

```
Db          7 CAGCAAC 1


RESULT 55
US-09-593-323-55/c
; Sequence 55, Application US/09593323
; Patent No. 6265213
; GENERAL INFORMATION:
;  APPLICANT:  Morgan, Antony R.
;  APPLICANT:  Severini, Alberto
;  TITLE OF INVENTION:  Compositions and Methods for Determining the Activity
;  TITLE OF INVENTION:  of DNA-Binding Proteins and of Initiation of
;  TITLE OF INVENTION:  Transcription
;  FILE REFERENCE:  DNAB-02921
;  CURRENT APPLICATION NUMBER: US/09/593,323
;  CURRENT FILING DATE:  2000-06-13
;  PRIOR APPLICATION NUMBER:  09/344,300
;  PRIOR FILING DATE:  1999-06-24
;  NUMBER OF SEQ ID NOS:  72
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 55
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-09-593-323-55

  Query Match             41.2%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCA 7
              |||||||
Db          7 CTCAGCA 1


RESULT 56
US-09-594-108-55/c
; Sequence 55, Application US/09594108
; Patent No. 6284468
; GENERAL INFORMATION:
;  APPLICANT:  Morgan, Antony R.
;  APPLICANT:  Severini, Alberto
;  TITLE OF INVENTION:  Compositions and Methods for Determining the Activity
;  TITLE OF INVENTION:  of DNA-Binding Proteins and of Initiation of
;  TITLE OF INVENTION:  Transcription
;  FILE REFERENCE:  DNAB-02921
;  CURRENT APPLICATION NUMBER: US/09/594,108
;  CURRENT FILING DATE:  2000-06-13
;  PRIOR APPLICATION NUMBER:  09/344,300
;  PRIOR FILING DATE:  1999-06-24
;  NUMBER OF SEQ ID NOS:  72
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 55
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-09-594-108-55

  Query Match             41.2%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCA 7
              |||||||
Db          7 CTCAGCA 1


RESULT 57
US-09-344-300-55/c
; Sequence 55, Application US/09344300B
; Patent No. 6297013
; GENERAL INFORMATION:
;  APPLICANT: Morgan, Antony R.
;  APPLICANT: Severini, Alberto
;  TITLE OF INVENTION: Compositions and Methods for Determining the Activity
;  TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
;  TITLE OF INVENTION: Transcription
;  FILE REFERENCE: DNAB-02921
;  CURRENT APPLICATION NUMBER: US/09/344,300B
;  CURRENT FILING DATE: 1999-06-24
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
US-09-344-300-55

  Query Match             41.2%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCA 7
              |||||||
Db          7 CTCAGCA 1


RESULT 58
US-09-101-272G-91/c
; Sequence 91, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
;  APPLICANT: Nissin Food Products Co., Ltd.
;  TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
;  FILE REFERENCE: Q50979
;  CURRENT APPLICATION NUMBER: US/09/101,272G
;  CURRENT FILING DATE:  1998-07-08
;  PRIOR APPLICATION NUMBER: JP 1059/1996
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 107
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: 5' end of HI-8 UTI DNA fragment (coding strand)
US-09-101-272G-91

  Query Match             41.2%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CAGCAAC 9
              |||||||
Db          8 CAGCAAC 2


RESULT 59
US-09-508-753B-61/c
; Sequence 61, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
```

```
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 61
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-61

  Query Match             41.2%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCA 7
              |||||||
Db         10 CTCAGCA 4


RESULT 60
US-09-508-753B-159
; Sequence 159, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 159
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-159

  Query Match             41.2%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTCAGCA 7
              |||||||
Db          1 CTCAGCA 7


RESULT 61
US-09-825-770-1/c
; Sequence 1, Application US/09825770
; Patent No. 6686180
; GENERAL INFORMATION:
;  APPLICANT: Blake, Milan S.
;  APPLICANT:  Bogdan, John A.
;  APPLICANT:  Nazario-Larrieu, Javier
;  TITLE OF INVENTION: Improved Method for the Production of
;  TITLE OF INVENTION:  Bordatella Pertussis Toxin
;  FILE REFERENCE: NV1933
;  CURRENT APPLICATION NUMBER: US/09/825,770
;  CURRENT FILING DATE:  2001-04-04
;  PRIOR APPLICATION NUMBER: 60/194,482
;  PRIOR FILING DATE: 2000-04-04
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: recombinant DNA
US-09-825-770-1

  Query Match             41.2%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TCAGCAA 8
              |||||||
Db          9 TCAGCAA 3


RESULT 62
US-10-677-496-1/c
; Sequence 1, Application US/10677496
; Patent No. 7018813
; GENERAL INFORMATION:
;  APPLICANT: Blake, Milan S.
;  APPLICANT:  Bogdan, John A.
;  APPLICANT:  Nazario-Larrieu, Javier
;  TITLE OF INVENTION: Improved Method for the Production of
;  TITLE OF INVENTION:  Bordatella Pertussis Toxin
;  FILE REFERENCE: NV1933
;  CURRENT APPLICATION NUMBER: US/10/677,496
;  CURRENT FILING DATE:  2003-10-03
;  PRIOR APPLICATION NUMBER: US/09/825,770
;  PRIOR FILING DATE: 2001-04-04
;  PRIOR APPLICATION NUMBER: 60/194,482
;  PRIOR FILING DATE: 2000-04-04
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: recombinant DNA
US-10-677-496-1

  Query Match             41.2%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TCAGCAA 8
              |||||||
Db          9 TCAGCAA 3


RESULT 63
US-09-263-790-23
; Sequence 23, Application US/09263790
; Patent No. PP12997
; GENERAL INFORMATION:
;  APPLICANT:  Nirmal Kumar PATRA et al.
;  TITLE OF INVENTION:   JAL PALLAVI, WATER LOGGING TOLERANT CYMBOPOGON WINTERIANUS
;  FILE REFERENCE:   2761-0120P
;  CURRENT APPLICATION NUMBER: US/09/263,790
;  CURRENT FILING DATE:  1999-03-05
;  NUMBER OF SEQ ID NOS:   38
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 23
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
```

```
;   OTHER INFORMATION: OPT 03 Primer - Used to develop the unique RAPD profiles of the
;   OTHER INFORMATION: plant Jal Pallavi
US-09-263-790-23

  Query Match             41.2%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 CACTCCT 15
              |||||||
Db          3 CACTCCT 9


RESULT 64
US-09-721-777-3
; Sequence 3, Application US/09721777
; Patent No. PP13279
; GENERAL INFORMATION:
;  APPLICANT: Khanuja, Suman Preet Singh
;  APPLICANT:  Kumar, Sushil
;  APPLICANT:  Shasany, Ajit Kumar
;  APPLICANT:  Dhawan, Sunita
;  APPLICANT:  Darokar, Mahendra Pandurang
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;  APPLICANT:  Singh, Anil Kumar
;  APPLICANT:  Patra, Nirmal Kumar
;  APPLICANT:  Bahl, Janak Raj
;  APPLICANT:  Bansal, Ram Prakash
;  TITLE OF INVENTION: Mint Plant Named Saksham
;  FILE REFERENCE: 033166-002
;  CURRENT APPLICATION NUMBER: US/09/721,777
;  CURRENT FILING DATE:  2000-11-27
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: OPT primer
US-09-721-777-3

  Query Match             41.2%;  Score 7;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 CACTCCT 15
              |||||||
Db          3 CACTCCT 9


Search completed: November 21, 2006, 14:30:59
Job time : 0.001 secs
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